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Human CARD 3 cDNA.

Human CARD 3 cDNA.

Haman RICK coding

Human cDNA 51-end

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   No.
          Score Match Length DB ID
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                   100.0
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                                                                      Human B1 cDNA. Ho
            1764
                    94.3
                            2024
                                       AAR16143
                                                                      CDNA sequence enco-
            1654
                   78.8
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                            2709
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	10	150	16.7	463	21	AAF21841	Human breast and o
	1.1	210	10.0	210	19	AAV33547	Clone 156108 cDNA
()	1.2	171	8.2	5.75	22	AAK93010	Human cDNA ∃' end
	13	4.9	2.3	:08	16.	AAT19776	Human gene signatu
	1.4	18	1.8	14.5	22	AAP64725	Novel human polynu
	15	18	1.6	2002	21	AAC79976	Human secreted plo
	16	+8	1.8	3 3 (1) 6)	21	AAA87701	Human secreted pro
	17	4.8	1.8	1.409	2.1	AAA87681	Human secreted pro
	1.8	+8	1.8	4.062	23	AAH+3347	Human colon cancer
	1.9	3.7	1.6	4	1.2	AA329008	CDNA encoding for
	20	37	1.8	236	2.3	AAK62412	Human immune∕haema
	2.1	47	1.8	396	222	AA187507	Buman polynucleoti
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	23	₹7	1.8	4.45	22	AAIHH908	Human polynucleoti
	24	+7	1.8	44 4	21	AAC59994	Human secreted pro
	25	37	1.8	470	22	AA182213	Human polynucleoti
	26	47	1.8	551	21	AACHU867	Human secreted pro
	27	3.7	1.8	386	1.86	AA191714	Rat SmillM, CEP2 CDN
	28	3.7	1.3	800	2.1	AACE 4708	Cmi.IM/CRP2 related
	29	₹7	1.8	880	2.2	AAD10427	Rat smooth muscle
	⊀()	₹7	1.8	36.6	20	AAX84947	Human secreted pro
(*	+ 1	+7	1.8	1.125	20	AAX30319	DNA encoding a hum
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	+4	+7	1.8	1602	2.2	AAS56395	Human cDNA for an
	3.5	47	1.0	المطأنط	211	AA719658	cDNA em odina a hu
	36,	×7).H	2197	21	AAC98120	Human colon cancer
	3.7	3.7	1.8	34.25	21	AAC178122	Human cancer assoc
	3.8	+7	1.8	3807	20	AAX37743	Human PRO326 DNA f
	39	47	1.8	4::53	20	AAX5-2266	Protein PROX26 ann
	4.3		* is	:		AAPENDAR	Human DE0326 pinto
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	; ;	3.7	7 2	4:553	2.2	AAF72424	Human PRO326 cDNA.
	4.4	57	1.8	1. 7:		AA-184422	Human PR0326 polyp
	15	17		1.1.		AAN NOTO	DNA coenciding for

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    AAY02578 standard 194A 2098 BP.
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     AAROUSSA
     אמי 1999 (first entry)
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DE
    Human Bl cDNA.
ΧХ
    Bigo being intra-climan mediator modulator inflammation, cell death;
     cell vurnical pathway intracellular signalling: AUS: cancer; human; ss.
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OS
     Homo sapiens
XX
PΝ
     WO9855507-A2.
XX
     10-DEC:1998.
PD
ХX
PF
     01 - JUN - 1998 :
                   98WO IL00255
XX
PR
     11-SEE 1997;
                    9711, 0121746
PR
     05-30N-1997;
                   9711.0121011.
     30-JUN 1997; 971L-0121199.
XX
    (YEDA ) YEDA RES & DEV CO LID.
λX
     Boldin M, Malinin N, Wallach D;
XX
     WEI, 1909 ST (250)/06
DK
DR
     P PSDB; AAW92795.
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New B. protein regulates cell death and cell survival pathways
           derivatives, DNA and antibodies, also regulate intracellular
           inflam chion, for freating AIDD, cameer
 XX
 103
            Avaim 1. Fig 3B; Supply English.
 XX
           this proceed to describes the asolation of a mover human Bl protein which
            on interact with, intracely a, ar mediators or modulators of inflammation,
           reil death'andZor cell sarvival pathways, directly or indirectly, dells
           can be modulated or mediated in intlammation, cell death or cell survival
          pathwass or another intracellular signalling activity using BL.
           Condit one sich as AIDS and cancer can be treated using BL. Antibodies,
           surgon spect, les and ribozymes can also be used to regulate the above
          test hwas a
 XX
           1. explore to 10 and BB 7. 64% Ap. 4522 (1) 44% (1) 56% The Depth theory.
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     Rest Local Similarity 100.0%; Prod. No. Cr.
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1861 actions itaasay at plaagiyaciyittti bagaagaaatgtgttloataaaagy 1920
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        1861 acttcaaaataaaaucatgtaagtgactgttttraagaagaaatgtgtttcataaaagg 1920
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     1921 ataris itatetetgittgettigaettittittata aaaateegtgagtattaaagettw 1980
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     1921 atattiatutototutteettitatata aaaatoogteagtattaaagottw 1980
     1981. awwraanykfotffshktaaataftagtotoootoratgacactgcagtattttttttau 2040.
         Dib
     1981 awwraar iktotttsiktaaatattagtotoootoratgacactgcagtatttttttaa 2040
     Db
     RESULT
    AAR49147 Standard, PDNA, 2024 BP.
    AAZ46143:
AC.
XX
    16-MAY-2000 (first entry)
DT
ХX
DE
    cDNA sequence encoding a human phosphorylation effector PHSP-6.
ХX
KW
    Human: phosphorylation offector, PHOP, proliferative disorder,
"KW
    immune disorder: neuronal disorder; ss.
ХX
OS
    Homo sapiens
XΧ
F'H
                  Location/Qualifiers
                  203...1825
                   /*tag a
FT
                   Perceduct "phisphorylation offector"
ХX
PN
    W020000€728:A2.
XX
    10-FEB-2000
ХX
     28 - IIII 1 444 -
                  99Wor-US17132
PF
ХX
PR
    28 .001 1998,
                  9808 0123494.
PR
    14-SEP-1998
                  98US-0152814.
     14 - OCT - 1998
                  98US-0173482.
     03-NOV 1998:
                  98US-0106889.
    19-NOV-1998
                  9805-0109093
PR
    22-DEC-1998;
                  98US-0113796.
PΚ
    12 - JAN 1999.
                  9903 0173482
    12-JAN-1999.
                 9905-0229005
XX
    (INCY:) INCYTE PHARM INC.
PA
ХX
    Hillman JL, Lal P, Tang YT, Corley NC, Guegler KJ, Baughn MR; Patterson C. Bandman \phi, Au-Young J, Gorgone GA, Yue H, Animual Y
PT
PI
PΙ
     Reddy R. Lu DAM, Shih LL:
XX
    WP1: 2000-183125/16.
1018
    P PUDB: AAY:8774.
DR
XX
    New human phosphorylation effectors use all for the diagnosis, treatment
PT
1/1
    and prevention of proliferative, immune and neuronal disorders -
XX
PS
    Claim 9; Page 121-122; 142pp; English.
ХX
     AAZ46138 Z46168 encode human phosphorylition effectors (PHSP),
CC
     designated PHSP1 PHSP31 (the protein sequence for PHSP28 is but given
CC
     in the specification). The sequences were isolated from cDNA libraries
CC
     prepared from various human tissues. The PHSP proteins are useful for
CC
     the diagnosis, treatment and prevention of proliferative disorders,
     immune disorders and neuronal disorders. The PHSP proteins form
    pharmaceutical compositions which useful for treating or preventing
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Himorders unseclated with decreased PHSE expression, Wetlivity. PHSP
        antagonists are useful for freating or preventing disorders associated
12/1
        with increased PHON expression/activity.
XX
30
        Sequence 2024 BP, (12 A, 445 ft, 434 d, 535 l) 2 other;
   Query Match 84.3%; Score 1769; DB 21; Length 2024; Best Escal Similarity 99.8%; Pred. No. 0;
   Matches 1919: Conservative
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             58 qfcaqctcfqqffcqqaqaaqcaqcqqcfqqcqtaqqccat.cqqqcaatqqqcqcctc 117
                  Db
               1 gtragetetggttrggagaagrageggetggegtgggreaterggggaaatgggegeete 60
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                   421 tagatttagitagattetteeaattttaggaatttgeaateageergaatttttgggaat 480
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            538 agttactgaatavatgovaaatgdatcattaaatgaa, tootavataagaaactgaata 597
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            836 yrracctyddaactulyaaccigyacaaaaatcaayyykkaytatkaagcacqatatata 897
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            781 gccaectgaaaactatgaacctggacaaaaatcaagggccagtatcaagcacgatatata 840
            896 Tagetatycayttatcaeatyygaaytyttatecayaaaacayccitttyaayatytcac 957
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                    1141 gttacagrafyfffeanglyceaftchecthfyfgheangaagaanatggaaffafefef 1200.
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                     3 CCL at it igaa rageteaagactgitatt! tatgaagetgeateactgteetggaaateacag 1380
            . 198-th phata praesath terggater caaaqqqer qeafter qrqateacaaqaccaetee. 1497
                    Lab
          138. It appartageacearther quarer canauquer qearterig rigar cacaaqaecactee 1440.
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          1558 tq ffataq-ocaqcaqtqqatccaqaqcaaaagqqaaqaattqfqaaccaaatqacaqa 1617
                    1 - 224-0 - 1081412121212121212121222222
           2.91 \pm i\,it\,it\,aa\,ree age agtiggatee agaage aaa aggigaaga cattgtigaace aaatga caga. 1560.
          1618 ag 59 goot taaccagt ogot agat good tict gt coagggact tigat cat gaaagagga, 1677
                    1971 as interest transcrapt eget agait recent et ut coaggaget tigat dat gagagaggg 1620
          3576 et il quaet l'yl bagt accaugect acauggacet cauuagt cagucuut fuct agucue. 1737
                    In 21 of at gracif this tags accompares acaming according manages carpaigness fract agains of 1680.
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                     t sousemunnaminininingmanihinininu.
          Torl to dipacal renaggagaagaattigesaaagtiafagtacaaaaattgaaagataacaa 1740.
          iller accounting for Coancertaice on a salar acting and the against account trade 1857
                    1/11 accumtagiletteagectluseeqquaatacttiftigqtttetagateaccaletttaaa 1800
          less this official and addicate that grade the transplacement of the cardinal section in the cardinal section is a second control of the cardinal section in the cardinal section is a second control of the cardinal section in the cardinal section is a second control of the cardinal section in the cardinal section is a second control of the cardinal section in the cardinal section is a second control of the cardinal section in the cardinal section is a second control of the cardinal section in the cardinal section is a second control of the cardinal section in the cardinal section is a second control of the cardinal section in the cardinal section is a second control of the cardinal section in the cardinal section is a second control of the cardinal section in the cardinal section is a second control of the cardinal section in the cardinal section is a second control of the cardinal section in the cardinal section is a second control of the cardinal section in the cardinal section is a second control of the cardinal section in the cardinal section is a section in the cardinal section in the cardinal section is a section of the cardinal section in the cardinal section is a section of the cardinal section in the cardinal section is a section of the cardinal section in the cardinal section is a section of the cardinal section in the cardinal section is a section of the cardinal section in the cardinal section is a section of the cardinal section in the cardinal section is a section of the cardinal section in the cardinal section is a section of the cardinal section in the cardinal section is a section of the cardinal section in the cardinal section is a section of the cardinal section in the cardinal section is a section of the cardinal section in the cardinal section is a section of the cardinal section in the cardinal section is a section of the cardinal section in the cardinal section is a section of the cardinal section in the cardinal section is a section of the cardinal section in the cardinal section is a sec
                    1801 firsette maataaaaqeatgtaaqtqactqtttteaaqaaqaaxtqtqttteataaa 1860
          1.e. agrafith at a confidencia da diffit frataga a confidencia da agrafica.
                    Per Lagra and transfer engine transfer and the contract of the
          1978 11 1979
         (1) (2) 1 (b) 1 (c).
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-AAC77779 standard: cDNA: 2709 BP.
хх
AC.
     AAC177779;
ΧХ
DT
     08 FEB: 2001 (first entry)
ХX
     Human cancer associated gene sequence SEQ 11-NO:173.
DE
XX
KW
     Human, cancer associated gene, cancer antigen, detection; cancer;
     diagnosis; cytostatic; proliferative; valuerary; immunomodulator;
KW
     antidiabetic; antiasthmatic; antirheumatic; antiarthritic; antiviral;
ΚW
KW
     antiinflammatory; antithyroid; antiallergic; antibacterial; cardiant;
     dermatological; neuroprofective; thrombolytic; coaquiant; nootropic;
KW
κw
     vasotropic; antipsoriatic; antianglogenic; gene therapy; inflammation;
KW
     immune disorder; haematopoietic cell disorder; autoimmune disorder:
KW
     allergic reaction; graft versus host disease; organ rejection;
     haemostatic; thrombolytic; cardiovascular disorder; intection;
KW
κW
     neurological disease; drug screening; ss.
ΧХ
OS
     Homo sapiens.
ХX
     WO200055450-A1
PN
ХΧ
     21 SEP-2000.
PD
ХX
     08 MAR-2000; 2000₩0 US05882
PE
XX
     12 MAR 1999; 99US 0124270.
PR
XX
     (HUMA:) BUMAN GENOME SOT INC.
PA
XX
     Rosen CA, Ruben SM;
11
ΧХ
     WPT: 2000-587533/55.
DR
     P PSDB; AAB43570.
DR
ХX
PT
     Novel isolated nucleic acids comprising sequences encoding peptides
     useful for treating or diagnosing e.g. cancer -
PT
ΧХ
     Plaim 1; Page 751 752; 2352pp; English.
PS
ХX
     AAC77607 to AAC78448 emode the human camer associated proteins given
CC
CC
     in AAB43398 to AAB44239. The proteins can have activities based on the
CC
     tissues and cells the genes are expressed in. Example of activities
170
     include: cytostatic; proliferative; vulnerary; immunomodulator;
     antidiabetic; antiasthmatic; antirheumatic; antiarthritic;
CC
CC
     antiinflammatory; antithyroid; antiallergic; antibacterial; antiviral;
CC
     dermatological; neuroprotective; cardiant; thrombolytic; coaquiant;
120
     mootropic; vasotropic; antipsoriatic and antianglogenic. The
     polynucleotides and polypeptides can be used for preventing, treating or
     ameliorating medical conditions and diagnosing pathological conditions.
CC
CC
     Polynucleotides, polypeptides, antibodies, auonists and antagonists from
CC
     the present invention may be used to treat immune disorders by activating
(20
     or inhibiting the proliferation, differentiation or mobilisation of
     immune cells, to treat disorders of haematopoietic cells, autoimmune
CC
     disorders, allergic reactions, graft versus host disease and organ-
(30
     rejection, modulate haemostatic or thrombolytic activity, modulate
CC
     inflammation, cancers, cardiovascular disorders, neurological disease and
     bacterial or viral intections. The peptides, nuclectides, antibodies,
:::0
CC
     agonists and antagonists may be also be used in drug screens. AAC78449 t:
CC
     AAC78457 and AAB44240 represent sequences used in the exemplification of
CC
     the present invention.
ХX
     Sequence 2709 BP; 810 A; 580 C; 540 G; 769 L; 10 other;
                          78.8%; Score 1654; DB zl; Length 2709;
  Ouery Match
  Best Local Similarity 99.7%; Pred. No. 0;
  Matches 1954; Conservative 0; Mismatches 6; Indels 0; Caps
```

20 grigging facigolog figginachagti totagaaaagaaqti ageti tagttiqaadaaqni 75

27 gragicyc tac gacyff tygcach ag firth tagaaaagaag can be fag fifeggadaag 🗀 🥳

Qy	80	##0990#1999############################	139
Db	87	ageggetggegtgggcatucggggaatggggecstogtgaeetagtgttgegggggeaa	
OY		aaagggtottgeeggeetegetegtgeaggggegtatetgggegeetgagegeggtgg	
Db		aaagggtottqooggeotogetogtgeaggggegtitotgggegootgaregeggegtgg	
QY nie		gadentt jägägnngnngnagnagnagnagnaenen jääänngsetgagngenngagnaen	
Db Og	207	gageettigggageegeegeageaggggeaeaeeeggaaeeggeetgagegeeegggaee	266 319
Qy Dh		atgaacggggaggceatctgcagcgccotgcccaccattccctaccaccacactcgccgac ffffffffffffffffffffffffffffffff	326
Qy		ofgrantacetgageogoggectotggcactgtytegtcogccogccacgcagctgq	379
Db		tillililililililililililililililililili	386
Qy		cqcqtinnaggtiggnngtigaagnanntignanatinna rantinngntigetegacagtigaaaga	
DЬ	387	$ \begin{array}{lll} & +11111111111111111111111111111111111$	446
Qy	440	aaggatgttttaagagaagetgaaattttacacaaagctagatttagttacatttttcca	499
Db	447		506
Оу	500	attttgggaatttgcaatqaqcctqaatttttggg;atagttactgaatacatgccaaat	559
Db	507	attttgggaatttgcaatgagcctgaatttttgggaatagttactgaatacatgccaaat	566
ÒУ	560	qqatcattaaatgaactcotacataggaaaactgaatatcctgatgttgcttggccattg	619
Db	567		626
ΩУ		agatttegeateetgeatgaaattgeeettggtqlaaattaeetgeacaatatgaeteet	
Db	627	agattteydatootgoatgaaattqooottggtgtaaattacotgoacaatatgaotoot	
Qy or		cctttacttcatcatgacttgaagactcagaalatsttattggacaatgaatttcatgtu	
Db Qy		cottracticateatgactigaagactoagaatatiitattiggacaatgaatttcatgtt	746
Db		aaqattgcaqattttigqtttatcaaaqtgqcqcat;atqtccctctcacaqtcacqaagt 	
Oy Oy		agonaatotgoacoaqaaqqaqqacaattattatatatacceeqqaaaactatqaacct	
Db	807	HITTHITTHITTHITTHITTHITTHITTHITTHITTHIT	
Ō.	96.0	gganiumiit maaggymagtat maagnangstatististisystutgisiyttiit <i>a</i> ija <u>ta</u> gg	919
Db	867		926
Qy	450	gaagtat tat chagaaaanageet EE qaagat gEraceaat eet EE geagat aat gEat	979
DЪ	927		986
Qу	980	agtgtgtcacaaggacatcgacctgtattaatgaagaaagtttgccatatgatatacct	1038
DÞ	987	agtigtigticacaaggacaticgacctgtitatitaatiga igaaagtitigecututigatatacct	104€
QУ	1040	canngageaegtatgatetetetaatagaaagtggstgggeacaaaatecagatgaaaga	1099
Db		caccgagcacgtatgatctctctaatagaaagtgg:tgggcacaaaatccagatgaaaga	
ΩУ		cost of the that a a a type the acting a a conjugate the type and	
Db	1107	ccatctttcttaaaafqfffaafaqaacffqaacfiqttttqaqaacatttqaaqaqata	1166

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1160 actitictiquagetqttatteagetaaagasaacaaagttacaagagtticaagtgcc 1219
Qy
      1167 artitictiqaaqctqttattcaqctaaaqaaaaaaaqttacaqaqtqttlcaaqtqcc 1226
   1220 altogortatgigacaagaagaagaatagaattatetetgaacatacetgiaattatatetatt
05
      1227 attoacctatqtqucuuqaaqaauatqqaattatetetqaasatacctqtaaatcatqqt 1286
   1280 ccacaagaggaatcalgiggatcctctcagctccatgaaaatagtggttctcctgaaact 1339
Qγ
      Db
   1287 cracaagaggaatcat.qtggatcctctcaqctccatgaaaatagtggttctcctgaaact 1346
   1340 toaaqqtoootaccaqctootcaaqaraatqattttttatotaqaaaaqctcaaqactqt 1399
      1347 toaaquteectaccageteeteagacaatgatttttatetagaaaageteaagactgt 1406
Db
   1400 tuttittatgaagetgeareacigteetggaaateaeagttgagatageaeeatttetgga 1459
      Db
   1407 tattitatgaagetgeateactgtoctggaaateacagttgggayageaceatttetgga 1466
   1460 tottcasaqqqctqcattctqtqatcacsaqaccactccatqctcttcaqcaataataaat 1519
Os
      1467 Intraaagggotgoattotgtgatoaraagaccactoratgotottragcaataataaat 1526
Db
   1520 praotiticaertgraggaartragaargtotgragrotggtatagoccagoagtggate 1579
Qy
      1527 ccacteteaactycaygaaacteagaacytetgcaycetggtatagcccagcagtggate 1586
Db
   QУ
      Db
Qy
   1640 gatqcccttctatccaqqqacttqatcatqaaaqaqqactatqaacttqttaqtaccaag 1699
      Db
   1647 gatgcccttctotccagggacttgatcatgaagggactatgaacttgttagtaccaag 1706
QY
   1700 cctacaaqqacctcaaaaqtcaqacaattactaqacactactqacatccaaqqaqaaqaa 1759
      1707 cctacaaggacctcaaaagtcagacaattactagacactactgacatccaaggagaaaa 1766
Db
Qy
   Db
Qy
   1820 ocqqqaaataottqtqqtttotaqatcaccatctttaaatttacttcaaaataaaaqcatq 1879
      Db
   1827 coqqaaatacttqtqqtttctaqatcaccatctttaaatttacttcaaaataaaaqcatq 1886
   1880 taaqtqactqtttttcaaqaaqaatqtqtttcataaaaqqatatttatatctctqttqc 1939
Ov
      1887 Laagtgactgtttttcaagaagaaatgtgtktcataaaaggatatttatatctctgttgc 1946
Db
   1940 Illigactittiitatataaaatccgtgagtattaaagctt 1979
      1947 tttgacttttttatataaaatccqtgaqtattaaaqctt 1986
RESULT 4
   AAK94554 standard; cDNA; 2033 BP.
AC
   AAK94554:
XX
L^{*}T
   -06 NoV 2001 (first entry)
XX
DE
   Human full-length cDNA, SEQ ID NO: 3453.
XX
   Human: full length cDNA: cDNA synthesis; oligo-capping; ss.
KW
ХX
OS
   Homo papiens.
ХX
   PP1130094-A2
PN
ХX
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A SHIP I.
  XX
              0.7 \ .001, -0.05 , while 0144089.
  1111
  XX
               TOWN TITLE (1997) 99, IP (1944) 86.
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  1. 87
               T. TAN 900: 2000 P.0118774.
                 or MAY or of committee LR Code.
  1130
  N.X
                CHELL, BELLX RES INCL.
  XX
                  " a L. Nishi∗awa i. Isogan L. Ha,ashi K. Ishii S. Kawai Y:
                Wikamatsi A. Suqiyama I. Naqii K. Kojima S. Sitsuki I. Koqa H;
  \mathbf{Y}, \mathbf{Y}
 1.4
                WELL 20 1 524:55/58.
 1.8
               P. USIDB: AAMSTOLIL.
  XX
 1-1
                Most Pricers useful for synthesizing full length cDNA clones and their
 1 : 1
                where in semestic manipulation.
  XX

    Fig. 1. May 1. No. (45 C. ) 600pp + sequence listing; English.

  XX
                The invention relates to primers for synthesising full length cDNA
                colores, also coNA molecules encoding a human protein have been
                isolated and nucleotide sequences of 5% and 3%-ends of the cDNA
              motocules have been determined. Primers for synthesising the full length
               CDNA are useful for clarifying the function of the protein encoded by
               the cDNA. The full length clones were obtained by construction of full
                length curiched cDNA libraries that were synthesised by the oligo-capping
              method. The primers enable the production of the full length cDNA easily
              without my special methods. The present sequence is a full length
                human of NA of the invention.
                Note: The sequence data for this patent did not form part of the printed
                specif: Pion but was obtained in CD ROM format directly from ERO.
               Sequence 2013 BP; 612 A; 447 C; 438 G; 536 F; 0 other;
                                                                           77.8%: Score 1632; DB 22; Length 2033;
       Query Mater.
       Best Local Similarity 99,7%; Pred. No. 0;
       Matches 1975 Coservative Or Mismatches 6: Indels Dr Caps
                      42 days to taliadagaagteagetet jalteggagaageageggetiggegtiggecateeg. 101
                                           set ermanteerrasionen astrinia iriiriin eri
 1.1
                         1. doi: first a managa agt caget et mit trada aga agraged greg tigger af eeg. 60
                   z_{\rm tot}/q_{\rm tot} and an independent and accelerated the equations are also also denoted by the z_{\rm tot}/q_{\rm tot}
                             1.4
                  \langle v \rangle_{c} that a radia eject at objugacycent alagographic gagagoof tigggagoog cagoliga i 221
                            3. Lorent in riggin and that of aggregate that aggregated for aggregated that aggregated aggregated in the control of the c
                   .... au l'intera di reconsquaresquest quaerquereqquaecat quaecqqqqqqqeat et qeal 281
                           zBT ad a paycacacterrequadecqueet quadequeeqqueeqa quadeqa quadeqaqaqaqaqa
                  282^\circ districtly intraction because as a additional to group a_i of a_i of a_i or a_i or a_i or a_i
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                   34.2 PCC of 490 s of 4154 bog for general crack caused danger great design frage cost assault. 401.
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                             Secretaria de la compania della comp
146
                   . 😘 Li aci it gcaco l'ecacact reget get egacagt gadagdaaggat gtict tidagagdagctig. 420
                  This admittitud reasagetagatitagtitaeattiffeeaattitgggaattigeaatgage 521
                            421 aautitti se aaagetagatttagttaeattetteeaattttgggaatttgeaatgage 480
: t
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Qγ		etgaatffffgggaatagftacfgaafacafgccaaafggateaffaaafgaacfccfac 581 	
Db		etyaatttiitgigaalagiilaetgaalaealgeeaaalggateallaaalgaaeleelae 540 -	
Оγ		ata qqaaa actgaatateetqatqttqettqqeeattqaqattteqeateetqeatqaaa 641 	
1)1)	54.1	aluyyaaaactyaatateetyatyttyettyyeeattyavattteseateetyeatyaaa (600 -	
ΨУ	64.2	-tlyccettyytytääättävetyvääääätälyäeteettetttäetteateatyäettyä 70); -{	
izb	601	. If general, Equipped and the entry extraordistic effects the efficient partitions $H(t)$.	
Ψÿ	702	agactcagaafafcffattggacaafgaafffcafqffangalfgcagaftffggfffaf 76} 	
Db	661	agacteagaatatettattqqacaatqaattteatqttaaqattqcaqattttqqtttat 720	
Ųγ	762	-caaagtqqcqcatqatqtccctctcacaqtcacqaaqtaqcaatctqcaccaqaaqqaq-821 	
Db	721	cauagtiggegeatigatigt coefict cacagticacquagtiag raquitict geoccagaaggas. 780	
$\forall \gamma$	822	qqacaattatttatatqccacctqaaaactatqaacctqqacaaaaatcaaqqqccaqta 885 	
de	781	ggacaattatotatatgccacctgaaaantatgaacctgaacaaaaatcaaqqqccaqta 845	
QΥ	882	teaageacqatafafafatagefafgeagffafeacafqqgaagfqffafecagaaaacage 941 	
Db	841	traagcargatatatatayetatgeagttatrararggggaagtgttatreagaaaarage 900	
Ογ	942	ettttqaaqatqteacebatcetttqeaqataatqtataqtqtqteacaaqqacatcqac 100}-	
Lib	901	ottittgäägätyteaccäateetttäcagaläalytatautytyteacaaugaeategac 960	
QУ	1002	etqttattaatgaagaaagtttgeeatatgatafaceteaeegageaegtafgafetete [196] -!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!	
DЬ	961	etgitattaatgaaqaaaqtifgeeatatgatataceteaceqaqcaeqtatqatetete 1020	
Ųγ	1062	taatagaaagtqqatqqgcacaaatccaqatgaaaqaccatetttettaaaatqtttaa 1221 	
Db	1021	taatagaaagtggatgggcacaaaatccagatgaaagaccatctttctt	
Ωy	1122	faqaacttqaaccaqtfftqaqqacattfqaaqaqataactfffctfqaaqcfqffatf;	
Db	1081	$tagaacttyaaccasttttspagaacalltgaagaagataactfttctlgaagclgttatts\ i14v$	
Оγ	1182	aqctaaaqaaasaaaqttacaqaqtytttcaaqtqccattcasctatqtqacaaqaaqa=1241 	
Db	1141	aqctaaaqaaacaaaqttacaqqqtqttcaaqtqccaftcacctafqfqacaaqaaqa 120%	
ΟУ	1242	aaatggaattateletgaacatacetgtaaateatgglecaraaqaagaateatgtggat 130} [[!!!	
Db	1201	auatgqaattatetetgaueataeetgtaaateatggteeacaagaggaateatgtggat. Let $(1,2,0)$	
υy	1302	ecteteageteeatqaaaataqtqqffeteefqaaactteaaqqteefqecagefeete 1961	
Db	1261	TCTFT TETT TETT	
υy	1362	aagacaatgattitttatetagaaaageteaagactgitattttatgaagetgeateaet 1425	
Db	1321		
Оγ	1422	qficct.qqaaatcacaqffqqqataqcaccafffctqqafctcaaaqqqcfqcaffctqfq [148]	
Db	1381		
υγ	1482	at cacaagac cactee at unit of the operation transfer out of case the aggregation $\{0,4\}$	
Db	1441		
Qy	1542	caqaacgtctqcaqcctqqtataqcccaqcaqtqqatccaqaqcaaaaqqqaaqacattq=1601	
Db	1501	$ \begin{array}{llllllllllllllllllllllllllllllllllll$	
Qy	1602	tyaannaatyanayaaynetyeettaaccayteyetayatyoottictytooayyyast 1661.	

127

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Db
     1561 tan menanataan igaaqeet qoot baaccagt og et agat good blot gbecagggact. 1620
     1662 frote it japagangaetatqaaettqttagtaee jageetacaaqqaeetcaaaaqtea 1721
         Db
     1621 tqutratgauuqaqqartatquacttgttagtaccuagectacaagqacctcaaaagtcu 1680
     1722 garmattantagapantantgapatresaggagaagaatttgebaaagttutugtubaau 1781
         Dis
     1681 garaattactagaractactgacatreaaggagaa aatttgetaaagttalagtacaaa 1740
     1782 ao ttangagataanaaacaaata na toti caaccita ceegaaaatan tuutgattiisi ja 1841
UV
         Db
    1741 aattqaaaqataacaaacaaatggqtetteageettaeeeggaaataettgtqqtteeta 1800
     1842 gatracratrittaaatttarittaaaataaaaqcatqtaaqtqactqttttteaaqaaq 1901
OΥ
         1801 gatcaccatotttaaatttaottoaaaataaaaocatgtaagtgactgtttttoaagaag 1960.
Db
     1902 auutginttivaraaaangatutiiatatototoitgottiganttittittatataaaat 1961
IJУ
         Db
     1861 aaatgiattirataaaaqqatatttatalototgiiqottigarttitttatataaaat 1920
     1962 coqtqaqtaffaaaqctt 1979
Ov
         1:7191 1481814141
     1921 coqtqaqtattaaaqctt 1938
RESULT 5
AAZU9246
H
    AA209246 standard, cDNA, 1931 BF.
ХX
    AA209246+
AC
XX
DI
    25-0CT-1999 (first entry)
XX
DE
    Human PARD - 3 cDNA.
ХX
KW
    CARD 3, caspase recruitment domain; CAR >-4; regulation; detection;
    caspass retinition, detection, screening, therapy, diagnosis, disease, apoptotic cell death; Pas/AFG 1 receptor complex, TNF receptor complex;
ΥW
KW
    cancer: follicular lymphoma; carcinoma; p53 mutation; viral intection,
\kappa_W
    hormone-dependent tumour; autoimmune disorder; Alzheimer's disease;
ΚW
    systemic lupus erythematosis: immuno-modiated glomorulonephritis; stroke;
κW
KW
    Parkinson's disease, amyotrophic lateral sclerosis, retinitis pigmentosa;
    spinal muscular dystrophy; herefullar degeneration, anaemia, dr.g. myelodysplastic syndrome; myecardial infarction; cell proliferation;
KW
KW
ΚW
    cell differentiation, cell survival, CARD 41, CARD 48, CARD 47,
KW
    CARD-42; human; ds.
XX
0.5
    Homo sapiens.
ХX
PH
    Kev
                   Location/Qualifiers
FΤ
    CDS
                   214...1836
FT
                   /*tag- a
FI
                   /product "CARD 3"
XX
    W0994 (102 A1)
PM
XX
    12-AUG 1999.
XX
    05-FER 1999;
                  99Wh-US02544
DE
XX
    08 DEC-1998;
PR
                  98US-0207359.
PR
    on FEB: 1998;
                  98US-0019942.
                  980S 0099041.
    17-JUN:1998:
XX
    (MILL-) MILLENNIUM PHARM INC
PA
XX
    Bertin J:
XX
    WPI: 1999-494269741.
DR
    P.PSDB: AAYH1140.
```

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PT
     regulation of cellular proliferation and differentiation and cell
     survival
XX
PS
    Example 2; Fig 1; 181pp; English.
хх
     This invention describes the inclution of movel human caspase recruitment domain, CARD + and CARD + polynoclectides and proteins and a
120
CC
     partial murine CARD-4L protein and genes. The genes and proteins of
     the invention are involved in the regulation of caspase activation.
CC
     The caspase recruitment domain (CARD) polynumiectides, pulypoptides,
CC
     homologues and antibodies can be used in screening assays, detection
     assays, predictive medicine and therapeutic and prophylactic methods of
     treatment. The methods may be used to diagnose and treat patients which
     are suffering from a disorder associated with abnormal level or rate of
CC
     apoptotic cell death, abnormal activity of the Fas/APO-1 receptor
     complex, abnormal activity of the PNF receptor complex, or abnormal
00
CC
     activity of a caspase. Diseases that may be freated include cancer
     (particularly follicular lymphoma, carcinomas associated with mutations
CC
     in p53 and hormone dependent tumours), autoimmune disorders (e.g.
     systemic lupus crythematosis, immune mediated giomerolonephritis), viral
110
     infections, Alzheimer's disease, Parkinson's disease, amyotrophic lateral
CC
     sclerosis, retinitis pigmentosa, spinal muscular dystrophy, cerebellar
CC
     degeneration, anaemia, myelodysplastic syndrome, myocardial infarction
     and stroke. CARD 3 protein interacts with other ceilular proteins, and so
    can be used for regulation of cellular proliferation and differentiation
     and cell survival. The CARD proteins may also be used to for screen drugs or compounds which modulate their activity. The CARD-4 deno can express a
     long transcript that encodes CARD 4L, a short transcript that encodes
     CARD 43 or two MARD 4 splice variants, CARD 47 and MARD 4Z. This sequence
CC
     encodes the human CARD 3 protein described in the method of the
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     invention.
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     Sequence 1931 BP; 613 A; 429 C; 416 G; 473 f; Cother;
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  Query Match 77.1%; Score 1617: DB 20: Length 1931; Best Local Similarity 59.7%; Fred. No. 0:
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    The present sequence is that of cDNA encoding human caspase
    recruitment domain 3 (CARD-3, see AAB20079). The cDNA was isolated
    tollowing a database search using known CARD sequences. Plasmid
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pXE17A containing CARD-3 obNA is deposited as ATCC 203037. CARE 3 700 is an intracellular protein predicted to be involved in regulating cuspase activation. It is useful as a rodulating agent in ac. regulating cellular processes include cell growth and cell death. CC Methods of diagnosing and treating patients suffering from a disorder associated with an abnormal letel or rate of apoptotic oc. co. I death, abnormal activity of the Fa /APA I receptor complex, cc abnormal activity of the tumour necrosis factor receptor complex CC or abnormal activity of a caspase involve administering a compound that modulates the expression or activity of CARD-3, CARD-4, CARD-5 or CAPO for qual small reterate, antise see nucleic acid, ribusyme CC or polypeptide. Such disorders include cancer, viral infection, autoimmune disorders, neurological diseases, haematological disorders, inflammatory disorders and immune disorders. CARD nucleic acids can be used to express CARD proteins in a host cell e.g. for gene therapy applications, to detect a genetic lesion and CC to modulate CARD activity. ХX Sequence 1931 BP; 613 A: 428 C: 416 C: 474 T, 0 other,

Query Match 74.6%; Score 1566; DB 22; Length 1931; Best Local Similarity 99.7%; Pred. No. 0;

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     . / AL. 1904.
                    enWorldSoeist
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     22 Alter Land
                    38118 00609023
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      TINMI , INIV MITHEIGAN.
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     Numez J. Inchara N. Koseki I:
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1.02
     WPT, 188 07,16 C/O6
    I PSDs AAY' 0404.
DR
XX
     Tompo. Prome for identitying apoptosis signalling pathway inhibitors
     useful for treating diseases.
111
XX
     Mainter: Fig. To, 93pp; English.
XX
     this perpence encodes the human RICK (RIP like interacting CLARP kinase)
    protein set the invention. The RDCK protein acts as a positive regulator
     of apoptosis potentialing apoptosis induced by caspase-8 and caspase-10
     during $195 signalling. The invention provides methods for identifying
     spopte its signalling pathway inhibitors and activators, and methods and
     compositions for screening compounds which will modulate the interactions
     of the various compositions identified: ARC, RICK, and the CIDE family of
     ectivators (TIDE A, CIDE B and DREP-1). RICK is useful in screening
     assays for adents, useful in the diagnosis, prognosis or freatment of
     disease associated with excess cell growth and dysregulation of
     apoptes and the applicates containing kink and chake can be used in drug
     sureer of assure to identity annihitor molecules blocking CD95-mediated
     apopto is, Oberexpression of Ake' in an in vitro cell system can be used
     the identity adminitors of the enzymatic activity of caspase 8.
     Identify rate a of ARC like inhibitory compounds may be useful for gene
     therap, treatment of disease with increased ceil death in muscle tissue
     But car had disorders. Therapeutic compositions of CIDEs can be used to
     front - i camer. Albs, neurodespendrative disorders, aplastic anaemia,
     machiner, a in cary, and toxin induced liver disease. AntiRICK antibodies
     in be used as respents for the preparation or affinity chromatography
    sela, and for diagnostically measuring RICK levels. A specific inhibitor
    of an electric step in the biochemistry of apoptosis is needed. RICK
     interaction with intracellular factors such as CLARP and FADD appears to
    to essential for apoptosis, inhabitors of RPCK binding to intracellular
     aparto, a factors are potential drap subdidates.
\lambda \lambda
    September 2502 BB; 769 A; 535 C, 495 G, 695 L, 6 other;
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72.4%; Score 1518; DB 21; Length 2502;
   Best Local Similarity 99.6%: Fred. No. 0:
                                                                    6: Indels 1: daps
   Matches 1938; Conservative 0; Mismatcher
          .36. yyr accayto totagaaaayaagtoago totyyttoygayaayoayoyyetyyetyyet
              I ggcaccaytetetagaaaaqaaqtcagctetagttegaaqaagaaqaaqcagctggcqtagac 600
Db
          96^\circ cationagagaat gaging continuont agript fransagagicaaaaaaaaaatit transaaa
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             аппантания попантичники сійна вый выбото бо
          6i categogyaatyggegeetegtgaeetagtgttgegggeaaaaagggteltgeeggei 20
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Uν
        . 156 - et cyclicytyc aggygr gtat et gygege tygg geggyget gagaget tyggage (af gylag) 21°
              121 integeticultycaydddiodati tyggedde byayegicu ayllyddageet fyddadeeur 186
Lit i
        -216 , egelagical gaggig calcalled elements of -276 , egelagical gagging and -276
QΥ
              -14b
        -181 - Equagraquqqqqaacacic qqaaceqqicefqaqeqcic aqqqaccafqaacqaqqqeca -240
        -276 tellgragingeri ligeriaricalleri Larraraaarti gergari ligegilari (1949) - 334
Uv
              [24] Tet gragegereat gereaceat beent accadaaan tii geogram geget accit gage (300)
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         335 legeggegent et gacact gtigt egt engenngchangact gangegt noaggtigann i 394
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              301 inappagnace to tagge act at a test este code code carge againt agree a treataget gales. 360
Dł
         395 graphical decay and the second of the second second quantity of the second seco
ΟV
             Dis
         361. głigawyca chi grama fichacach thorgotych cyanagi gawygawyga tyfici tawyw 420.
        455 gaagetgaaattttaeacaaagetagatttagttacattttteeaaltttgggaatttge 514
Οy
              Db.
        421 qaaqetqaaattttaeacaaaqetaqatttaqttacattetteeaattttqqqaatttac 480
        515 aatgageetgaattittigggaatagttuctgaataeatgeeaaatggateattaaatgaa 574
UV
               481 aatgageetgaalttttggggaatagttaetgaataeatgeeaaatggateattaaatgau 541
Db
        575 et cet acat aggaagact gaat at cet gat gt t get t gecat t dagat t t egeat eet g -634
OV
             Ob
        541 ctrictae ataggaaaa elgaatalee tyatgityettyye caltigagattie geateerig 600
        635 catgaaattgeeettggtgtaaaltachtgearaatatganterfortttacttcatcaf 694
ÚУ
             601 catgaaattgcccttggtgtaaattacctgcacaatatgactcctcctftacttcatcat 660
[ pt :
        695 gacttgaagactcagaatatcttattggacaatgaatttcatgftaagattgcagafttt 264
Οy
              Db
        661 ganttgaggantnagaatatottattgganaatgaatttnattgttaagattgnagatttt /20
OV
        755 qqtttatcaaaqtqqcqcatqatqtccctctcacaqtcacqaaqtaqcaaatctqcacca 814
              721 qqtttatcaaaqtqqcqcatqatqtccctctcacaqtcacqaqtaqcaaatctqcacca 78
140
        815 qaaqqaaqqaa qaltatttatatqccacctqaaqactatqaacctqqacaaqaatcaaqq-874
Ųγ
             781 qaaqquqqaaattatetatatqeeacetqaaaactatqaacetqqacaaaaateaaqq 840
Db
        875 gerpagtat baagcacgat at atat aget at geagt tat bacat gggaagt gt tat beag i 1994
ΟV
             Dit.
        841 genagtathaageacgatatatatagetatgeagtiathacataggaaagtgtiatheaga 900
        1935 - aaacageet tit tigaagat gil caccaat.cet titigeagat aat git at agligt eacaagga 1994
Uγ
             901 adacageettitgaagatgteaceaafeettigeagataatgtatagtgteteacaagga 96
Dh
        995 categacetyttättäätyäägäääytligeealalyafaiaeeteaeeyäyeäeytälä 1054
OΥ
             961 inaltogametyllfaftaatgaagaaagtttgodatatgatatacetoadegagdacytat\sigma / 1 \ll
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1055 at high the ataqua antiquat qquana aa ate: agat gua aga ceateittettu au 1114
       1621 at ct. tot aataqaaaqtagatqqacacaaaatc. aqatqaaaqaccalctttettaaaa 1080
    ill5 tqtttaafaqaacttqaaccaqttttqaqaacat!tqaaqaqataacttttcttqaaqct 1174
ŲΨ
        Dh
    1081 tqtttaataqaacttqaaccaqttttqaqaacatttqaaqaqataacttttcttqaaqct 1140
    1175 qttattnaqetasaqaaaacaaaqttacaqaqtctttcaaqtqccattcacctatqtqac 1234
        1141 gitattcagctaaagaaaaaaattacaqagtgittcaagtgccattcacctatgtgac 1200
Db
    1235 angaagawantgqaattatototgaanatacotgraaatnatggtocanaagaggaatna 1294
27
       <u>ទី គឺម៉ែលអំពីពីពីពីពីពីពីពេកអត់</u> រយៈអេពីសាកាសែវិការៈ
    1201 a mangagagattggggttatototgggggattgcotg agateatggtocacagaggggatca 1260
Db
    1295 tytiquaticeteteageticeatgaaaatagtggti iteetgaaaetteaaggteeetgera 1354
       1261 figriggation of cagoticoat gasastagtiggt: stoctgaaactteaaggteectgeva 1320
Db
    1355 gotoot taaqamaatqattiittatotagaaaaq oteaaqaetgitatiitatgaaqetg 1414.
        314181.121411841846
Db
    1321 getectedagaraatgattttttatetagaaaagiteaagactgttattttatgaagotg 1380
    1415 catcactqtcctqqaaatcacagttqqqataqcarcatttctqqatctcaaaqqqctqca 1474
QУ
        1381 catcactgtcctggaaatcacagttgggatagcalcatttctggttctcaaagggctgca 1440
Db
    1475 ittictiqtiqaticacaaqaccacticcatiqcti (titicaq caataa),aqaticcacticticaactiqca, 1534
Qy
       suktinuukikumahaminahininininanahinin
Db
    1441 ttotqtqafraraaqacvactocatqotettrascaataataataaatoogototoaaotqoa 1500
    15.95 gradiant hagalangt of gradient get at agency agrangt gg at heagaginan aggg gall. 15.94
Q٧
       1501 qqaaactcaqaacgtotycujectqqtataqeecagcagtggatecagagcaaaaaqqaa 1560
    1595 decattorgaaccaaatgacagaagcetqeetts accagtegetagatgeeettetgtee 1654
Qy
        Db
    1561 qacattqtqaaccaaatqacqaaqectqcctt:accaqtcqctaqatqccttctqtcc 1620
QY
    1655 agggant Egaticatgaaagaggantatgaactti ttagtaccaagcotacaaggacctica 1714
         1621 agggacttgatcatgaaaqaggactatgaacttottagtaccaagcctacaaggacctca 1680
    1715 adagt dagadaat tadtagadadan tiqaqato maaqqagaaqaatt tiqadaaqt tala 1774
       Db
    1681 awaqt cagacaattactayacar tactgacatc aaqqaqaaqaatttqccagaqttata 1740
    1775 qtaraakaattgaaaqataacaaacaaatgqqtiittcaqccttarccqqaaatacttqtq 1834
        1741 utacaaaaattgaaagataacaaacaaatgggt ttcagccttacccggaaatacttgtg 1800
    1835 gttfctagafcaccafcfffuaafffacttcaalataaaaqcafqtaaqtqactgttttt 1894
Qy
        Db
    1801 qttictagatcaccai ritthaatttastt aasatsaaaq atqtaaqiga tuttiti 1807
\cup y
    1895 caaqaayaaatytgtttoataaaayyatatttatatototgttyotttyacttttttat 1954
       1861 caaqaaqaaatgtqtttcataaaaaqqatattt/talctctqttqctftqucttttttttt. 1920
    1955 atabaatcoqtqaqtattaaaqott 1979
ŲУ
       atemania manamana an a
    1921 utuauatoogtgagtattaaagott 1945
RESULT 8
   AAK92259 standard; cDNA; 740 BP.
XX
AC
    AAK92259:
ХX
   06-NOV-2001 (first entry)
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```
Human cDNA 5' end sequence, SBQ 1D NO: 719.
XX
      Human, full length codA, codA synthesis, eligo capping; ss.
Eiv
XX
      Homo sapiens.
ХX
      EP1130094-A2.
PN
XX
PD.
      05 SEP-2001
ХX
₽T,
      -07 JUL 2000; 2000EP-0114089.
       08 ЛИ.-1999; 9-ЛР-0194486.
1110
       11-JAN-2000; 2000JP:0118774.
DR
7110
       02 MAY 2000, 2000JP-0183765.
ХX
       (HELI'S) HELIX RES INST.
PA
ХX
P!
      Ola T. Nichikawa I. Icemai T. Hayachi K. Ichii F. Kawai Y:
       Wakamatsa A. Saqijama i. Naqai K. Kojima S. Otsaki i. Koga H:
VΧ
       WPT: 2001-524255/58
DR
XX
PΤ
       830 Primers useful for synthesizing full length cDNA clones and their
      use in genetic manipulation
ХX
      Claim 2, SEQ ID NO 719, 1380pp / sequence listing; English.
228
       The invention relates to primers for synthesising full length cDNA
      clones, 830 cDNA molecules encoding a human protein have been
       isolated and nucleotide sequences of 5' and 3' ends of the CDNA
CC
       molecules have been determined. Primers for synthesising the full length
       comA are useful it: clarifying the function of the protein encoded by
       the CDNA. The fall length clones were obtained by construction of full
       length enriched offNA libraries that were synthesised by the oligo capping
       method. The primers enable the production of the full length cDNA easily
       without any special methods. The present sequence is the nucleotide
       sequence of the 5' end of a cDNA provided in the invention.
       Note: The sequence data for this patent did not form part of the printed
      specification, but was obtained in CD ROM format directly from EPO.
CC
ХX
      Sequence 740 BP: 179 A; 193 C; 200 G; 164 F; 4 other;
                                     22.3%; Score 468; DB 22; Length 740;
   Best Local Similarity 99.6%; Prod. No. 2.60-.74;
  Matches 568; Conservative 0; Mismatches 2; Indels 0; Gaps
          45 ctictaqaaaaqaaaqtcaqctctqqtticaqaqaaqcaqcaqctqqcqtqqqccatccqqqq-104
              Db
            Tiletetagaaaaqaaqticaqotictggtticggagaagcayoggictgg.qtgggcatioaqqquibU
27
         TL
          61 aabqqq,qeriteygtyalebaqtabbqqqqqqq,aaaaaqqybbbbqqqqeqb,qetqqt-120
         QY
              il 21 gelagggggt at litigggrope tig agegeggggt gaggget tig gage i de gelage ag 180
ijЬ
        225 gaqqaaaaccaqaaaccaqoot qaqcqqqqqqqqqqqqqqqqqqqqqqqqqtcatctqqqqqqq-284
QΥ
              181 guggacaccegguacegge, tgagegeeeruggaaccatgaarguggaggeeatetgeageg 240
1.b
        . 285 (real favorales ratios estas acadas bogos das objects taes bigadocyclydddolft, . 344

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              241 contagendary at their take as adapting engagety great transferage grand grand some
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         345 integrant at at cathodic equal coloridate a cathodic a cath
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              Db
         301 etggeactglateatengeengeeaggagaetgggggtenaggtggeegtgaagnace 360
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405 il a rachat relicaeret ceget get egacagt galaagaalaggat gtit titaagagaaget galaai 464
           14
      151 it a sacat ecacact coqet qet equicaqt qaaaqaaaqqat qtict taaqaqaaqct qaaai 420
      465 Cliftac icalaagetagalfiagttacattitteeaafttigggaattigeaatgageetg 524
            4.21\% tt accreasage tagat tragt tarattet treesaft traggast traggast argecty. 480
14.
      1.25 - iut 1.17 ggaat agt tact gaat acat gecaaat ggat cat taaat gaact cet acata. 584
          481 - 6411111 gguatagt fact gaat scatgecasat ggat cat tagat gaactectacata - 540
: t
       95 Januari quatatechquiqit qet ngqc 614
            zon vincemarenen era
      541 gaaaaastgaatateetgatgttgettgge 570.
PERMIT :
AAK935.24
    AAK95 24 standard; cDNA, 740 bi-
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A.
     AAKS C 24
XX
     96 Nov 2001 (first entry)
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. 4E
     graman of NA colorer representative sequence, SEQ To NO: 1984.
XX
KW
     guman (til, .ength cDNA: cDNA s, thesis; oligo capping; as.
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     malio , ipoetis
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    3321130 64 A.
EN
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190
     the SEE Indial
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111
     ** JUL 10900 2000 BP 0414 089.
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     . н. 101: 1 сов; — эвдр отв44кы,
1112
PR
     11 JAN 2000; 20000HP 0118774
     AMAY 20000; 20000TP 0183765.
1.16
XX
PΑ
     CHELL , HELLY RES INST.
XX
111
    eta T. Nishikawa I. Isoqai i. Hayashi K. Ishii S. Kawai Y.
111
     Wakamat to A. Suqiyama I. Naqii K. Kejima S. Otsuki T. Koga H:
XX
     WELL 2001 524.555/58.
, 1Fe
XX
21
     800 Primers useful for synthesizing full length cDNA clones and their
     case in genetal manipulation.
XX
     Example 11; SEQ 1D No 1984; 1380pp + sequence listing; English.
XX
     The insertion relates to primers for synthesising full length cDNA
    cleanes 200 cENA molecules encoding a human protein have been
    restated and nucleotide sequences of 5% and 6% ends of the CDNA
     anotecution have been determined. Primers for synthesising the full length
     SENA are useful for clarifying the function of the protein encoded by
    the cDNA. The tull length clones were obtained by construction of tull
     remath excited cDNA libraries that were synthesised by the oligo capping
    method. The primers enable the production of the tall length cDNA easily
     without any special methods. The present sequence was used as the
    represe tative sequence from a human clone which was used in
    homolog, searches to identity the clone.
    Note: Le sequence data for this patent did not form part of the printed
     specification but was obtained in the ROM format directly from EPO.
XX
     September 148 each 179 At 193 Ct 2000 Str 164 Tt 4 other).
  pared . Matters
                         22.3%. Stree 468: 168-22: Length 740:
  Rest Schar Samilaraty Sec. 66; Prod. No. 2.66 174;
 Matches for a precivative or Mismatches 2: Indels 6: Gaps
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QΥ
      .45. et et agaaaagaagt.caget et ggf t eggagaageagegget ggegt ggeegt eggeeat eegggg. 184
        A of chaqaaaqaaqA caqchingqB chaqabin qaaqaaqC aqchiqC qB qaqC at C C C C
[5].
     105 - aallyggegeeet egit gaeet agt git gegyggeaaaaaggyt et t geeggeet eget egit - 164
ÚУ
        Db
      61 aat gagggeeet egt gaeet aat git geggggeaaaaagggt et t geeggeet eget eat. 126
     165 acagagagat at cit aggicgicot gago godgogt gagaacoot rigagago oyo oyo agcada 224
ОV
        121 gradgggraf at Chagacacaf gagcacaf gradgade et tigagade eu cacadcada. 189
Db
     225 i qqqcacaec eqqaac eqqect qaqciqci eqqqac catiqaac qqqqaqqecat et qcaqcq-284
Ūγ
         Db
     181 gaggaracccqqaaccqqcctqaqcqccqqqaccatqaacqqqqqccatctqcaqcq 240
     285 , equity occurred the quity accuracy and the quarter of 446
UΥ
        Die
     241 inceptige dealerat tiedet aledae aaachtegeegaelet geget ale it gagelegegegeget ii. 8057
ÚУ
     345 ottageactigtigticative qui equi vai quagae tiga acqitocadgitageogtigaagcano. 494
        301 of agraet gligting ting concern can an again tyging of incarput garing tigal agrain (6.0)
(d)
     405 tgcacatecacactecgetgetegacaglgaaagaaaggatgttlaagagaagetgaaa 464
OV
        Db
     361 tydgeatiddae Eddyetydfegaeagtgaaagaaaggatyfettaagagaagdaggtgaso 420
     465 Itttacacaaaqctagatttagftacafttffccaaffitgggaarffgcaafgagccfa 524
ΟV
         42) tittacacagaggitagattlagitacalictlicaatt!!taggaa*!tigcaatgagcctg 480
inb
     525. aaftittigggaatagtiacigaatacaigccaaalggaticallaaatgaacicclacata (584
ÚУ
        481 aattittigggaatagtiacigaatacaigcaaaiggalcailaaaigaacicciacaia 540
Οy
     585 ggaaaactgaatateetgatgttgettgge 614
        Db
     541 qqaaaactqaatatcctqatqttqcttqqc 570
RESHLT 10
AAF21841
ID AAF21841 standard: DNA: 463 BP.
ХX
    AAF21841;
AC.
ΧХ
    27 MAR 2001 (first entry)
DT
ΧХ
    Human breast and ovarian cancer associated antigen gene SEQ ID 228.
DE
ΧХ
    Human; breast cancer; ovarian cancer; cytostatic; immunosuppressive;
ĽW
    montropic; neurpprotective; untiviral; untiallergic; hepatotropic;
KW
    antidiabotic; antiintlammatory; antiulcor; vulnerary; anticonvulsant;
ĸw
    antibacterial; antifungal; antiparasitic; cardiant; immune disorder;
KW
    Addison's disease; allergy; autoimmune haemolytic anaemia:
KW
    autoimmune thyroiditis; diabetes wellitus; Crohn's disease;
    multiple sclerosis; rheumatoid arthritis; blockative colitis;
KW
    cardiovascular disorder; wound healing; neuro logical disease; ds
KW
XX
08
    Homo sapiens.
ХX
    W0200055173 Al
PΝ
XX
P15
    ⇒1 SEP 2000
XX
    08-MAR 2000; 2000WO US05881.
DF
XX
PR
    12 MAR 1999; 9908 0124270.
ХΧ
FΑ
    (HOMA ) HUMAN SENOME SCI INC.
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Rosen CA. Ruben SM;

1 : 1

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WPI: 2:00:611515Z58
Dk
    P-PSDB; AAB58938.
DR
ХX
PT
    New human breast and ovarian cancer associated gene sequences and the
PΤ
    polypeptides encoded by these genes, useful in the prevention.
PT
    treatment and diagnosis of cancer, immuse disorders, cardiovascular
PΤ
    disorders and neurological diseases -
XX
PS
    Claim 1; Page 653; 1299pp; Poglish
ХX
CC
    Sequences AAP21614 AAP22031 represent DNA sequences encoding human
CC
    proteins AAB58711 - AAB59128. The DNA and protein sequences are
    associated with breast and ovarian carrer. Included in the invention are sequences AAF22032 - AAF22040 and AAB$(129 which are used in the isolation and characterisation of the LNA and protein sequences of the
CC
QC.
    invention. The breast and ovarian came r associated DNA, protein, agonist
ĆĊ.
    or antagonist sequences exhibit cytostatic; immunosuppressive;
CC
    nootropic; neuroprotective; antiviral, antiallergic; hepatotropic;
CC
    antidiabetic; antiintlammatory; antiqueer; vulnerary; anticonvulsant;
    antibacterial; antirungal; antiparasitic and cardiant activity. The
    polynucleotide and protein sequences are used in the diagnosis of cancer,
CC
    particularly breast and ovarian cancer The nucleic acid sequences,
    proteins, agonists and agonists may also be used in the diagnosis,
ćc
    prevention and treatment of immune disorders e.g. Addison's disease,
CC
    allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis,
    diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatoid
    arthritis and alcerative colitis, cardiovascular disorders such as
ge
ee
    myocardial ischaemias; wound healing; neurological diseases such as
    cerebral anoxia and opilopsy, and infectious diseases.
    Sequence 462 BP; 150 A, 92 C, 89 C, 111 T, 1 other,
 Query Match 16.7%; Score 350; DB 21, Length 463; Rost Local Similarity 44.6%; Pred No. 5 40-128;
  Matches 450; Conservative 0: Mismatches
                                               2: Indels 0: Caps
     546 aatacatgocaaatgqatcattaaatgaacto-tacataggaaaactgaatatcctqatg 605
          Db
       1 aatamatgomaaatggatmattuaatgaacto tacatugguuduut juututootjuty 60
Qy
     606 itigotiggecatigagatitogcaticotqcatigaattigecettqqtqtaaattacetqc 665
         61 | ftgcttggcaftgagatttcgcafcctqcaf jaaattgcccttggtgfaaattacctqc | 120
Db
     666 acaatatqactcctccttacttcatcatcatgac;tqaaqactcaqaatatcttattqqaca 725
ΟV
         121 acaatatqactceteetttaettoatcatgacttqaaqactcagaatatettattggaca 180
Db
      726 - ar gaatht cat git ba galt gcagaitt biggtit at calagt ga ca catgaligi 2. Liet - 725
OY
         stitustui mintiniattiiaanniiiaanniiiaanni
Db
      181 utqaatttcatgttaaqattqcagattttqqtttatcaaaqtqqcqcatqatqtccctct 240
      786 managtrangaagtagnaaatotgnacoagurggaggacaattatttatutyvuulity 845
97
         Db
      241 managthangua (tagnaaatotgoacoaga: qqag )qabaattatotatatqubuchty 300.
ÚΥ
      846 aaaantatqaachtqqacaaaaatcaaqqqneaqtatcaaqnanqatatatatataqetatq 905
         Db
      301 aaaactatgaacctggacaaaaatcaaqggc aqtatcaaqcacqatatatataqctatq 360
      906 rayttalcacatgggaagtgl.talccagaaa.icagccttt.tgaagatgtcaccaatcctt. 965
OV
         einamiiinii wama airananinaana
Ob
      361 caqtiatcacatqgqaagtqktatccaqaaascaqccttitqaaqatqtcaccaalcctt 420
QY
      966 tgcagataatgtatagtgtgtcacaaggaca: 997
         Db
      421 tgcaqataatqtataqtqtqtqacaaqgacat 452
RESULT 11
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AAV33547
    AAV33547 standard; CDNA; 210 BP.
1.15
XX
     AAV33547;
XX
101
     29 DEC: 1998 (first entry)
XX
    clone 156108 cDNA fragment encoding a human protein kinase homolog.
DE
ΧХ
ΚW
     Protein kinase: cell signalling: inflammation; carcinoma; diabetes;
    human X linked agammagrobulinaemia, nonspherocytic hacmolytic anaemia;
FW
    arthorosclerosis, glioma, restenosis, chotera based septic shock;
     001064 Dictyostellam Y kinase; ss.
XX
    Home sariens
08
ХX
    US5817479-A.
PN
XX
    06-0CT 1998.
PD
XX
PF
    07-AUG-1996;
                  9646-0200525
XX
PR
    07 AUG-1996; 96US 0700575.
ХX
PA
    (INCY ) INSYTE THARM INC.
XX
    As Young J. Bandman to Hawking PR. Wilde CG:
1.1
XX
DR
    WELL 1998 516307/47.
ХX
PT
     Human kinase polynmeteotide(s) and recondinant products - useful
PT
     for identification of modulators of the enzyme, and treatment of
     discuses associated with abnormal kinase expression.
XX
    Claim 1; Columns 45 48; 30pp; English.
E/S
XX
     The invention provides polynomicotides which come is morel protein.
CC
    Richard homelogs expressed in various bamas solle and tissues. The
00
    present sequence represents the clone 156108 cDNA fragment derived from
    a human cDNA library designated THE 1 phorbol LES. The cDNA encodes
    a protein kinase which shows homology to the AAU01064 Dictyostelium Y
CC
    kinase. Verter, and heat calls can be used for recombinant production
    of the protein kiname homolog. The recombinant proteins may be used to
     raise antibodies for use as anti-kinase therapeuties. Eligenuelectides
    based on the polynucieotide sequences, i.e. probes and antisense
00
     constructs, the poptides and antibodies are claimed to be useful as
CC
     tools for studying signalling cascades in colis and proteins, and for
     identifying inhibitors (drugs) to treat dispases and inflammatory
CC
     conditions associated with abnormal kinase expression. Diseases that
     are claimed to be treatable include human X tinked agammaglobulinaem.a.
CC
     nonspherocytic baemolytic anaemia, artheroscierosis, carcinomas,
     diubétes, gliemus, refiteresis, chileru banca nepti sebilib, et
ΧХ
    Sequence 210 BP; 74 A; 40 C: 41 G; 55 1; 0 other:
                         10.0%; Score 210; DE 19; Length 210;
 Query Match
 Boot Local Similarity 100.0%, Fred. No. 6.2e 73:
  Matches 210; Conservative 0; Mismatches 0; Indexs 0; Saps
      844 tqaaaactutqaacctggacaaaaatcaaqqaccaqtatcaaqcaqatatatatagctu 903
          I fydadactutgaucciggucaaaaatcaaggacagtatcaagcacgatatatatacacta 66
Dh
      904 tyraqttatearutqqqaaqtqttateeaqaaaaruqeettttqqaaqatqteaecaatee 963
QУ
          Db
       6) tgcaqttatcacatqqqaaqtqttatccaqaaaaacaqccttttqaaqatqtcaccaatcc 120
QΥ
      964 ttiqqaqataufqtutaqtqtqtqcaqaqqqaqatqqa retqttattaatqaaqaaqqtti 1023
          TRI KIR KILIR KANTAR KATULAR K
      121 Ittgragatautgtutaatattaraaaggarategaretgttättaatgäägääägftt 180
     1024 gecatatgatataceteacegageacgtat 1053
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0.001 | 0.001 | 0.001 | 0.001 | 0.001 | 0.001 | 0.001 | 0.001 | 0.001 | 0.001 | 0.001 | 0.001 | 0.001 | 0.001 | 0.001 | 0.001 | 0.001 | 0.001 | 0.001 | 0.001 | 0.001 | 0.001 | 0.001 | 0.001 | 0.001 | 0.001 | 0.001 | 0.001 | 0.001 | 0.001 | 0.001 | 0.001 | 0.001 | 0.001 | 0.001 | 0.001 | 0.001 | 0.001 | 0.001 | 0.001 | 0.001 | 0.001 | 0.001 | 0.001 | 0.001 | 0.001 | 0.001 | 0.001 | 0.001 | 0.001 | 0.001 | 0.001 | 0.001 | 0.001 | 0.001 | 0.001 | 0.001 | 0.001 | 0.001 | 0.001 | 0.001 | 0.001 | 0.001 | 0.001 | 0.001 | 0.001 | 0.001 | 0.001 | 0.001 | 0.001 | 0.001 | 0.001 | 0.001 | 0.001 | 0.001 | 0.001 | 0.001 | 0.001 | 0.001 | 0.001 | 0.001 | 0.001 | 0.001 | 0.001 | 0.001 | 0.001 | 0.001 | 0.001 | 0.001 | 0.001 | 0.001 | 0.001 | 0.001 | 0.001 | 0.001 | 0.001 | 0.001 | 0.001 | 0.001 | 0.001 | 0.001 | 0.001 | 0.001 | 0.001 | 0.001 | 0.001 | 0.001 | 0.001 | 0.001 | 0.001 | 0.001 | 0.001 | 0.001 | 0.001 | 0.001 | 0.001 | 0.001 | 0.001 | 0.001 | 0.001 | 0.001 | 0.001 | 0.001 | 0.001 | 0.001 | 0.001 | 0.001 | 0.001 | 0.001 | 0.001 | 0.001 | 0.001 | 0.001 | 0.001 | 0.001 | 0.001 | 0.001 | 0.001 | 0.001 | 0.001 | 0.001 | 0.001 | 0.001 | 0.001 | 0.001 | 0.001 | 0.001 | 0.001 | 0.001 | 0.001 | 0.001 | 0.001 | 0.001 | 0.001 | 0.001 | 0.001 | 0.001 | 0.001 | 0.001 | 0.001 | 0.001 | 0.001 | 0.001 | 0.001 | 0.001 | 0.001 | 0.001 | 0.001 | 0.001 | 0.001 | 0.001 | 0.001 | 0.001 | 0.001 | 0.001 | 0.001 | 0.001 | 0.001 | 0.001 | 0.001 | 0.001 | 0.001 | 0.001 | 0.001 | 0.001 | 0.001 | 0.001 | 0.001 | 0.001 | 0.001 | 0.001 | 0.001 | 0.001 | 0.001 | 0.001 | 0.001 | 0.001 | 0.001 | 0.001 | 0.001 | 0.001 | 0.001 | 0.001 | 0.001 | 0.001 | 0.001 | 0.001 | 0.001 | 0.001 | 0.001 | 0.001 | 0.001 | 0.001 | 0.001 | 0.001 | 0.001 | 0.001 | 0.001 | 0.001 | 0.001 | 0.001 | 0.001 | 0.001 | 0.001 | 0.001 | 0.001 | 0.001 | 0.001 | 0.001 | 0.001 | 0.001 | 0.001 | 0.001 | 0.001 | 0.001 | 0.001 | 0.001 | 0.001 | 0.001 | 0.001 | 0.001 | 0.001 | 0.001 | 0.001 | 0.001 | 0.001 | 0.001 | 0.001 | 0.001 | 0.001 | 0.001 | 0.001 | 0.001 | 0.001 | 0.001 | 0.001 |
               The great at gat at acct caccgagg aggrapt at 1210.
REPORTED IN
AAF GOLO --
           -AAK - sold of instand; CDNA; 575 BP
XX
             AAK -- 13-
XX
101
           -06-NeV 2001 (first entry)
XX
1.4
            number (DNA 3) end sequence, SEQ 1D Not 1470.
XX
KW
            Framer's tol. length sDNA; sPNA synthesis: oligo capping; ss.
XX
             iiome staputence.
ХX
FN
            EP1 - 6-94 Ad.
XX
111
              objects to good,
XX
PE
            5753 1 200 : 2000EP 0114089
196
             1985; 1966 #8.Hr 0194486
1116
            T1:37 N 2006 20 00JP 0118774
             OBSMAY DOD - BOOOMP OTBRIGHS
ХX
             (HEL. ) HELLX RES INSI.
i·Λ
XX
              da I. Nistikawa I, Isogai I, Hayashi K, Ishii S, Kawai Y;
1.1
            Wakar it u A - Shqiyami I. Naqil K. Kollimi S. Pitsuki I. Koqu H;
XX
            White could firefactive.
Like
XX
             you increasuseful for synthesizing tull length cDNA clones and their
1.1
111
             use in genetic manipulation.
XX
             Craim 3: SEc ID NO 1470: 1380pp + sequence listing: English.
125
XX
             the invention relates to primers for synthesising full length cDNA
             Stames, 800 SDNA molecules encoding a human protein have been
             isolated and nucleotide sequences of 5' and 3' ends of the CDNA
            molecules have been determined. Primers for synthesising the full length
             DNA are asseral for clarifying the function of the protein encoded by
            the ciNA. The full length clones were obtained by construction of full
            liengt: earliched PDNA libraries that were synthesised by the oligo capping
            method. The primers enable the production of the full length coma easily
             without any special methods. The present sequence is the nucleotide
             sequence of the C end of a cDNA provided in the invention.
             Note: to sequence data for this patent did not form part of the printed
              specifications but was obtained in CD ROM format directly from EPO.
XX
              Segment to 574 BPS 173 As 106 (t) 30 to 195 Is 11 others.
                                                                    (8.26) Score 171; DB 22; Length 575;
      grant Matt.
    Best Toda Similarity (198,5%) Fred. No. 1.16 57;
    Matches .'T: 'mservative 0: Mismatches 0: Indels 0: Caps 0:
            1809 ft bageettaeeeggaaataettgtggtttetagateaeeatetttaaafttaetteaaa 1868
                               THE TABLE TABLE TO A SECOND REPORT AND A SECOND REPORT OF THE PARTY AND 
            (1903) at unuacidat autouctofittiteaugaugaat (tattealuaaaggatatitat (1928
                          т за Болинений Враний Синдиний Вилинг
               🗆 🥕 A BAAAGGA GAAGGAAGAC GA LILILI O AAGAAGAAA IGTGTTTCATAAAAGGATATTTAT. 146
            . Com as it is a reget to gaze this situata sa a a a a consignificant a a agent in 1979.
                             s ar s desenerences erektableariere
               545 A TELIGREGOLEIGACHERTTTATATATAAAAFOGTGAGTATTAAAGGTT 95
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RESULT 13
AA:19776
    AAT19776 standard: cDNA to mRNA: 198 RP
XX
    AAT19776;
Ar'
XX
DT
    12 JUL 1996 (tirst entry)
ХX
DE
    Human gene signature HUMGS00852
XX
    Gene signature; messenger RNA: mRNA; relative abundance; frequency;
KW
     human; cloning; mapping; non-biased library; diagnosis; detection;
KW
    cell typing; abnormal cell function: ss.
XΧ
    Homo sapiens.
OS
XX
    WO9514772 Al.
PN
ХX
    01 JUN:1995.
PD
ХX
PF
    11-NoV-1994; 94Wo-JP01916
ХX
     12-NoV-1994; 93JP-0355504
PR
XX
    (MATEZ) MATEURARA K.
PA
    (OKUBZ) OKUBO K.
PA
ХX
PI
    Matsubara K, Okubo K;
XΧ
    WPI: 1995-206941/27.
DR
ΧХ
127
     Identitying gene signatures in 3' directed human cDNA library (e.g.,
     for diagnosis of abnormal cell function, by preparing cDNA that
DT
117
     reflects relative abundance of corresp. misNA in specific human
     tissues
ХX
PS
    Claim 1; Page 469; 2245pp; Japanese.
ХX
CC
    A single stranded DNA (or its complementary strand or the corresp.
CC
    double-stranded DNA) which comprises one of the 7837 "GS" sequences
CC
    given in AAT19001 T26837 and which is able to hybridise to part of
CC
    human genomic DNA, cDNA or mRNA is claimed. The GS (Gene Signature)
    sequences were obtained from 3' directed cDNA libraries prepared
CC
    from various human tissues; synthesis of cDNA was initiated from the
CC
     3' end of manA by using pol_3(\tilde{t}) as the sole primer. Since the \tau'
cc
    untranslated sequence is unique to a particular mRNA species, almost
ce
    all the 3' oriented cDNAs hybridise with specific mRNAs. Each library
CC
    is constructed so as to reflect accurately the relative abundance of
ge.
    different mRNAs in the particular tissue from which it was derived.
ac
    The appearance frequency of a given of in a cDNA library can be
    determined (esp. using primers and probes derived from the GS
1363
    sequences) as a means of diagnosing abnormal cell function or fire
CC
    recognising different cell types.
ΧX
    Sequence 108 BP; 36 A; 14 C; 13 G; 39 1; 6 other:
  Odery Match
                          2.3%; Score 49; DB 16; Length 108;
  Best Local Similarity 100.0%; Pred. No. 1.1e 09;
  Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
     . 1886. uetgititteuugaugaaigigitteulaauggalaittutaletet. 1934.
          45 actqttttcaaqaaqaaatqtqtttcafaaaaqqafafffatafctct 93
Db
RESULT 14
ID AAF64725 standard: cDNA: 349 BP.
ΧХ
    AAF54725;
AL:
    19-APR-2001 (first entry)
DT
```

```
Novel tuman polynaciectide, SEQ ID No. 481.
DE
AA
      Human; cytostatic; gene therapy, colon cancer, prestate cancer,
ĸw
      breast cancer; lung cancer; cancer detection; ss.
KW
\mathbf{x} \mathbf{x}
PΝ
      W0200102568-A2.
F-1 :
      11-JAN-2001.
XX
      30-JUN-2000; 2000WH-9818374.
PF
XX
      02-JUL-1999: 9908-0142310.
PR
      02-301-1999; 9908 0142311.
PR
ХX
PA
      (CHIR.) CHIRON CORP.
      (HYSE-) HYSEQ INC.
ХX
      Williams LT. Escobedo J. Innis MA. Garcia PD. Klinger J. Kassam A;
Feinhard C., Rondazzo F. Kennedy GC. 1 J. D. Lamson G. Drmanac R;
grkenjakog K. Drmanac S. Dickson M. Lukat I. Leshkowitiz D:
D-T
D 1
PI
      Kita D. Gardia V. Jones LW. Strache-Crain B;
XX
      WP1: 0001-001905/10
DR
XX
PT
      Library of polynucleotides for diagnosing a cancerous state of a
      mammalian cell and detecting cancer, particularly of the colon or
PΤ
      prostate, comprises 3351 human polynucleatide sequences -
XX
PS
      Claim 9; Page 613; 1046pp; English.
CC
      The present sequence is one of 3351 sequences in a library of human
      polynucleotides. The library is used to detect differentially expressed gones correlated with a cancerous state of a mammalian cell and can
dd
dd
      detect colon, prostate, breast and lung cancer. The library can be used
CC
      to produce probes for detection of meNA and to produce additional copies
CC
      of the polynucleotides. The probes can be used for chromosome mapping of the polynucleotide and for detection of transcription levels. Ribozymes or antisense oligonucleotides can be generated. The polynucleotides and
CC
CC.
      their gene products are used as genetic or biochemical markers (e.g. in
CC
      blood or tissues) that will detect the carliest changes along the
      carcinogenesis pathway and/or monitor the efficacy of therapies and
      preventine interventions. The polynuclectides, polypoptides and
      antibodies against them can be used in pharmaceutical compositions to
      treat the cancers and proliferative disorders such as needlasia,
      dysplasia and hyperplasia.
ХX
      Sequence 349 BP; 126 A; 70 C; 58 G; 95 1; 0 other;
SU
  Omery Match 1.89; Score 48; 3B 22; Length 449;
Host Local Fimilarity 100.08; Bred. No. 20 05;
Matches 38; Conservative 0; Mismatches 0; Indels
                                                            0; Indels 0; Caps
      2061 aattigasaaaaaaaaaaaaaaaaaaaaaaaaaaa 2098
            247 aattigasaaaaaaaaaaaaaaaaaaaaaaa 284
Di
RESULT 15
AAC79976
      AAC79976 standard; cDNA; 2082 BP.
XX
AC.
      AAC79976 -
ХX
      12 FEB-2001 (first entry)
XX
      Human secreted protein encoding cDNA for gene 29.
DE:
      Secreted protein; human; immunosuppressize; antiarthritic; antirheumatic;
KW
      antiproliterative; cytostatic; cardiant; vasotropic; corebroprotective;
```

```
nootropic; neuroprotective; antibacterial; virucide; fungicide;
      ophthalmological, valnerary, gene therapy; treatment; autoimmune disease;
hyperproliferative disorder; cardiovascular disorder; ocular disorder;
cendrovascular floorder, herayor system disorder; hitertions skin adina;
EW
       wound healing; epithelial cell proliferation; transplantation; ss.
KW
XX
       Homo sapiens.
      W0200058357-A1.
PD
       05 oct 2000.
       23 MAR 2000: 2050WO-US07723.
PE
XX
       26-MAR:1999; 99US-1126506.
PR
       07 JAN 2000; 200000 0174952.
12.12
XX
PA
       (HUMA ) HUMAN CENOME SCI INC
XX
       Rosen CA, Ruben SM. Komatsoulis G:
       WP1: 2000-611704/58
DK
1000
       PERSON AAB45053
ХX
       Nucleic acid moleciles encoding haman secreted proteins, used in
Pil
       proventing, treating a realignating a disorder e.g. Alzheimer's and
127
Dit
       Parkinson's diseases and cancers
ХX
       Claim la; Page 356 357; 418pp; English.
       This invention describes novel isolated nucleic acid molecules (I)
       encoding a human secreted proteins (11) which have immunosuppressive,
      encoding a human secreted proteins (II) which have immunosuppressive, antiarthritic, antirhomatic, antiproliferative, cytostatic, cardiant, wash repic, condecipent extive, next repic, neuroprotective, antibacterial, virially, family, and pathologists, and an be used for gene therapy. (I) and (II) are used to prevent, treat or anchirate a medical condition in e.g., behaves, wice, rabbits, quasts, horses, cats, days, whicheas or sheep (I) and (II) are also used in diagnosing a pathological condition or susceptibility to a pathological condition. The antibacles to (II) can also be used in alloying symptoms associated with the disorders and in diagnostic immunosassays at a conference of a covered links of languages at a conference and conferences as a covered links of languages and assays (IL)(SA).
       eld, tadividuomeassays or coryse linked ismonescribent assays (BLISA).
       Disorders which are diagnosed or treated include autoimmune diseases
       egg, chemmatered arthritis, hyperproditionative disorders e.g. neoplasms
       of the breast or liver, cardiovascular disorders e a, cardiac arrest.
       cerebrovascular disorders e.g. cerebral ischemia, angiogenesis, nervous
       system disorders e.g. Alsheimer's disease, infections coused by bacteria, viruses and tengi and ocular disorders e.g. corneal infection. The
       polypeptides can also be used to aid wound heating and epithelial cell
       preliferation, to prevent skin aging due to sumburn, to maintain organs
       before transplantation, for supporting cell culture of primary tissues,
CC
       to regenerate tissues and in chemotaxis. The polypeptides can also be
       used as a food additive or presentive to increase or decrease storage
1262
XX
       Sequence 2082 RP: 588 A; 460 C; 423 G; 611 I: 0 other:
  Oncery Match ...8%: Score 38; DB 21; Length 2082; Best Local Similarity 100.0%; Pred. No. 1.60:05.
                38; Conseivative 0; Mismatches
                                                                        0. Indels 0: Caps
       2061 aatttgaaaaaaaaaaaaaaaaaaaaaaaaa 2098
109
               2029 aatttgaaaaaaaaaaaaaaaaaaaaaaaaa 2066
Search completed: May 1+, 2002, 21:31:01
Job time: 8577 sec
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.

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Result

OHERV

Score Match Length DB ID

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GenCore version 4.5
                 Copyright (c) 1993 - 2000 Compagen Ltd.
OM nucleic - nacleic search, using sw model
Run on:
                May 14, 2002, 19:04:21; Search time 4997.99 Seconds
                                           (without alignments)
                                           8784.306 Million cell updates/sec
Title:
                US-09 445-22+-2
Perfect score:
                2098
Sequence:
                Scoring table:
                Gapop 60 0 . Capest fe.s.
Searched:
                1797656 segs, 10463268293 residues
Word size :
Total number of hits satisfying chosen parameters:
                                                    3595310
Minimum DB seq length: 0
Maximum DB neg length: 2000000000
Post-processing: Listing first 45 summaries
Database :
               GenEmbl:*
               i: qb_ba:*
               2: qb_htq:*
               3: qb_in:*
               4:
                  gb_om:*
                  gb_ov:*
               6:
                  gb_pat:*
                  qb_ph:*
                  qb_pl:*
                  gb_pr:*
               10: gb_ro:*
               ll: qb_sts:*
               12: qb_sy:*
               13: qb_un:*
               14: qb_vi:*
               15: em_ba:*
               16: em_fun:*
               17: em_hum:*
               18:
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               19: em_mu:*
               20: em_om:*
               21:
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               29: om_vi:*
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               31: em_htg inv:*
               32: em_htq_other:*
               33: em_htgc_inv.*
     Pred. Mr. in the number of results predicted by chance to have a
     score greater than or equal to the score of the result being printed,
     and is derived by analysis of the total score distribution.
                                 SUMMARIES
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Description

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                        2098 6 A82777
                                                             BC00455 ← Homo sapi
                        1898 9 RCD34554
          1719
                 81.9
                                                             AX082199 Sequence
          1668
                 79.5
                        1931 6 AX082199
                                                             AF027706 Homo sapi
          16.44
                 78 i
                         2501 9
                                  AF027706
                                                             AFU64824 Homo sapi
          1570
                 74.8
                         1902 9
                                  AF064824
                                                             AF0785+0 Homo sapi
          1.4.1.9
                 67 6
                        1623 9
                                  AF078530
          1416
                 67 5
                        1626 6
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           439
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                              9 HSM802204
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                   1 8 164907
                                  AC007146
                                                             ACUU7146 Drosophil
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                         346 9
                                                             AK026649 Homo sapi
                                  ARREST ACTOR
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                                                             AK026542 Homo sap.
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                                                             AP418663 Brassica
                         823 8
                                 AF4 1356 C
            3.7
                          862 10 80010316
                                                              BC010316 Mus muscu
            3.7
                         880 6 ARL36617
                                                             ARI36617 Sequence
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    29
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                          880 fi
                                  AR162055
                                                             AR162055 Sequence
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                         1266
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                                                             AP236856 Pribolium
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                                                             AF052159 Homo sapi
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                         1479
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                                  AX255868
                                                             AX255868 Sequence
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    17
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                                  AF459587
                                                             AF459587 Lotus jap
    38
                  1.8
                         1596
                                  AX330553
                                                             AX330553 Sequence
                  1.8
                         1301
                                                             X74801 H.sapiens
    4.0
                         1901
                                  HSHUMAPC
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   4.1
                  1.8
                         1902
                         1954
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            37
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                                                             BC018736 Homo sapi
                        2106
   43
                  1 H
            37
                        2345
                                  AB060888
                                                             AB060888 Macaca ta
    44
                  1 H
                              1.4
                        2744 9 HSM801975
                                                             AL137663 Homo sapi
    15
                                     ALIGNMENTS
RESULT
A82777
Locus
            A82777
                                                         linear PAT 21-JAN-2c00
                                     20008 bp
DEFINITION Sequence 2 from Patent W09855507.
ACCESSION
VERSION
            Δ82777.1 31:6732464
KEYWORDS
SOURCE
            unidentified.
 ORGANISM
            unidentified
            unclassified
REFERENCE
            1 (bases 1 to 2098)
 AUTHORS
            Boldin, M. and Wallach, D.
            MUDDINATORS OF INTRACTINGUAR INFLAMMATICAL THAT DEATH AND CELL
  TITLE
            SURVIVAL FATHWAYS
            Patent. W: 9855507 A 2 10 DEC-1998;
  JOUENAL.
            BOLDIN MARK (IL); WALLACE DAVID (IL)
PEATURES
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                     /organism "unid∈ntified"
                /organism unique cirred
/db_krct "taxon:32644"
649 a 452 c 449 a 539 t
BASE COUNT
                                                       9 of hers
ORIGIN
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ыb	1861	ACAAAATCCAGATGAAAGACCATCTETCTTAAAATGTTTAATAGAACTTGAACCAGTTTT 124	
IJγ	1141	gaqaacatttgaagaqataacttttettgaagetqttatt sagetaaaqaaaacaaaqtt [2200 	
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114)		AATGGGTCTTCAGCCTTACCCGGAAATACTTGTGGTTTCLAGAECACCAECTTTAAATLL 1800	
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01)		ATATTTATATCTCTGTTTGACTTTTTTTATATAAAATCCGTGAGTATTAAAGCTTW 1:000	
07		awwraargkte!!!srkiaaatattagteteeeteeatgacactgcagtatt!!!!ttaa 2040 !	
Di		AWWRAAROKICITISKKIAAALALLAGICICCCICCAIGACACIGCAGIATTITTITIAA 2040	
Οy		Häätacaagtaaaaagttgäätttgaaääanaaaäääa sanaaäaaaanaaäääaaa 2098 	
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COMMENT
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                     DNA Sequencing by: National Institutes of Health Intramural
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                     Web sites
                                                http://www.niscorih.gov/
                                                nisc_mqc?nhgri.t.lh.gov
                     Contact:
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Benjamin,B., Blakesley,F.W., Bortford,C.G., Brinkley,C., Brooks,Y.,
Dietrich,N.L., Guan,X., Gupta,J., Ho,S.-L., Karlins,E., Legaspi,R.,
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                     McDowell, J., Pearson, R., Snyder, E., Stantripop, S., Thomas, P.J.,
                     Tiongson, E.E., Touchman, J.W., Tsirgeon, C., Vogt, J.L., Walker, M.A.,
                     Zhang, L.-H. and Green, E.D.
                     Clone distribution: MGC clone distribution information can be found
                     through the I.M.A.G.E. Consortion CINE at

    http://www.link.gov.

                     Series: IRAL Plate: 15 Row: n Column: 18
                     This clone was selected for full length sequencing because it
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                                     POPPOSETECT TELEPVIPTERE CONTRACTORER TELOSVASSATALCORREMETS IN
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ORIGIN
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               850 TAGCTATECAGTTATCACATEGGAAGTGTTATCCAGAAAACAGCCTTTTGAAGATGTCAC 909
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                T. SO GUACAGAGIGITICAAGIGCCAIICACCIAIGIGACAAGAAAAAGAAAAIGGAATTAICICI IZO9
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                 1270 AAALAGIGGIRCIGCIGAAAGIICAAGGICCCIGGGAAGAICAAGAAAAAATATTTT 1329
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    (bases 1 to 1931).

     AUTHOR:
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JOHRNAL.
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            Imohara, N., del Peso, L., Koseki, T., Chen, S. and Nunez, G.
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            RICK, a novel protein kinase containing a caspase recruitment domain, interacts with CLARP and regulates CD95-mediated apoptosis J. Pirl. Chem. 273 (20), 10096-10090 (1008)
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           Thome M Hofmann K . Burns.K., Martinon, F , Bodmer, I -I.,
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           Identification of CARDIAK, a RIP lke kinase that associates with
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           Curr Riol 8 (1998) In press
REFERENCE
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           Mattmann, C. and Tschopp, J.
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                             Medarthy, L.V., Ni, J. and Dixit, V.M.
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                                  Biol. Chem. 274 (27), 16968-16975 (1998).
                              DC (1) / 9 ().
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REFERENCE
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    AUTHORS
                           Bertin.J
                           Novel molecules of the eard related protein family and uses thereof
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                           Fatent: Wo 0100826-A 3 04 JAN 2001;
                           Millennium Pharmaceuticals, Inc. (US)
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                  Mammala: Entherra: Primates: Catarrhin: Hominidae: Homo.
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                     reisky, P., Holmes, A. and Broy, M.
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                    the sequence of Homo sapiens BAC clone CTA 4371.15
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                    Shmitted (21 DEC 1999) Repartment of Genetics, Washington
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                        Center: Washington University Genome Sequencing Center
                        intention worder WHGSR*
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NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

This sequence was finished as follows anless otherwise noted: all regions were double stranded or sequenced with an alternate chemistry; an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.

MAPPING INFORMATION:

This chromosome 8 clone was provided by Dr. Patrick Concannon (patcongymmc.org) at the Virginia Mason Research Institute.

SOURCE INFORMATION:

Clone CTA-437L15 is from a release of the homan BAC library CITB-HS-A. The library contains cloned DNA from homan sperm. See: Shizuya et al., Proc. Natl. Acad. Sci. USA 89:8794-7 (1992): U.L. Kim et al., Genomics 34:213-8 (1996). The clone is available from kesser: h Genetics, Inc. (http://www.reagen.com). VECTOR: pBeloBAC11

Selection: chloramphenicol

NEIGHBORING SEQUENCE INFORMATION:

/codon start-1

The clone sequenced to the left is CTA 237GL. The actual start of this clone is at base position 1 of CTA:4371.15; actual end is at 116650 of CTA:4371.15.

This clone contains STS HS275YF1 (NID:q1051703).

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/evidence not_experimental

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RESULI 9
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DEFINITION
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VERSION
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REFERENCE 1 (based 1 to (20250)
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AUTHORS
           Filation, M. and Varon, R.
  TILLE
            icross Submission
            Submitted (30 DEC 1998) Senome Analysis, Institute of Molecular
  THURNAL.
            Brotechnology, Reutenbergstrasse II, Jena 07745, Germany
COMMENT
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REFERENCE
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          Au-Young, J., Bandman, O., Bawkins, P.R. and Wilder C.G.
 AUTHORS
 TELEVILLE.
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PEACURILI
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REFERENCE
          1 (bases 1 to 1352)
          McCusker.J.H.
 AUTHORES
 TITLE
          Identification of five amino acid biosynthesis genes from the human
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 JOURNAL
          Unpublished
          2 (bases 1 to 1352)
REFERENCE
 AUTHORS
          McCusker.J.H
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 JOHRNAL
          Submitted (26 JUN 2001) Microbiology, Dake University Medical
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Senter, Research Drive, Darham, NC 27710, USA
FEATURES
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eESU() 12
H2016 / 8 36
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AMEINITEON CHOMO Applens htra. beta 2 mENA, complete cis.
A TOPEGLE IN THE 78 OF
VERSI N
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KEYWHELES
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MERKINGE.
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   JOHLENAL.
                      NA Cell Biol. 16 (6), 679 690 (1997).
   MEDICALINE
                     (1355E3)
FEFFERN 'F

    (bases 1 to 420)

   AUTH RGS
                     werl, B., Screaton, G. and Stamm, S.
                     areast Submission
                      superfied (30 JAN 1997) Maximinsk institute for Phychiatry, Am
   J. JURNAC
                     Flipferspitz 18 a. Planegg 82152. Germany -
 EAT19-1
                                   - Location/Qualitiers
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VERSION
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REPERENCE
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 AUTHORS
           Williams, L.T., Escobedo, J., Innis, M.A., Garcia, P.D., Klinger, J.,
           Kassam, A., Reinhard, C., Randazzo, F., Kennedy, G.C., Pot, D., Lam.on, J., Jananae, K., Cikenjako, E., Dreara, S., Ed. Fson, M.
           Labat, L., Leshkowitiz, D., Kita, D., Garcia, V. and Strache Crain, E.
           Human denes and dene expression products
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           Patent: WO 0102568-A 481 11-JAN 2001;
 JOURNAL
           CHIRON CORPORATION (US) : HYSEQ, INC. (US)
PEATURES
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REPERENCE
           1 (bases 1 to 992)
 AUTHORS
           Strausberg, R.
  TITLE
           Direct Submission
           Submitted (12 JUN 2001) National Institutes of Health, Mammafian
  JOURNAL.
           Gene Collection (MGC), Cancer Genemics office, National Cancer
           Institute, el Center Drive, Room 11A0:, Bethanda, MD 20892 2590.
           NIH-MeM Project Web: http://mqc.nci.nih.gov
Contact: MGC help desk
 PEMARK
COMMENT
           Email: cqapbs-r@mail.nih.gov
           Tissue Procurement: DCTD/DTP
           cDNA Library Preparation: Rubin Laboratory
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           Web with a high process the suite of
           Contact:
                         nisc,mgc⊴nhqri.nih.qov
           Shevehenko, Y., Wetherby, K.D., Beckstrom: Sternberg, S.M.,
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Benjamin,B., Blakesley,R.W., Bouttard,G.G., Brinkley,C., Brooks,S., Dietrich,N.L., Guan,X., Supta,J., He,S.-L., Karlins,E., Legaspi,R.,
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            Zhang, L.-H. and Green, E.D.
            Clone distribution: MCC clone distribution information can be found
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             Series: IRAL Plate. 20 Row. b Column. 16
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            Identification of a liver specific cDNA clone chaperoning the
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  JOURNAL
            Unpublished
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  AUTHORS
  TIPLE
            Direct Submission
  JOURNAL.
            Submitted (06-APR-2001) Departamento de Biologia Molecular,
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Job time: 8735 sec
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GenCore version 4.5 Copyright (n) 1992 2000 Compages Ltd. OM protein - protein search, using sw model Run on: May 13, 2002, 21:/1:05 ; Secreb time 93.63 Seconds (without alignments) 997.728 Million cell updates/sec US-09-445-223-1 Title: Perfect score: 540 1 MNCEATHEALPTIPYHELAD......PEILVVSKSPSLNLLONESM 540 Sequences Scoring table: Gapop 60.0 , Gapext 60.0 Searched: 562222 segs. 172994929 residues Word size : Total number of hits satisfying chosen parameters: 562222 Minimum DB set Length: 0 Maximum DB seq length: 20000000000 Post-processing: Listing first 45 summaries Database : SPIREMBL_19:* 1: sp_archea:* 2: sp_bacteria:* 3: sp_tungi:* 4: sp_human:* 5: sp_invertebrate:* 6: sp_mammal:* 7: sp_mhc:* #: sp_organelle:* 9: sp_phage:* 10: sp_plant:* 11: sp_rodent:* 1. sp_vis.s • 13: sp_vertebrate:* 14: sp_unclassified:* 15: sp_rvirus:* 16: sp_bacteriap:* 17: sp_archeap:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SHMMARIES

kesult No.	score	- * - Qiery - Match	Length DB	11)	Description
1	4.51	35.4	540 4	04 3 3 5 3	O43353 homo sapien
2	1.0	1.9	54 5	○17541	017541 caenorhabdi
4	1)	1.9	29 i 11	Q9D685	Q9d685 mus musculu
4	i 1	1.9	517 5	Q21292	Q21292 caenorhabdi
Γ,	1.)	1.9	582 5	018645	018645 drosophila
6	1 -)	1.9	678 5	09 V 306	Q9v3q6 drosophila
7	1.0	1.9	697 13	рчиже2	290x-2 brachydani:
H	1.)	1.9	698 11	Q91284	091xr4 mus misculu
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1 %	,	1.7	55 10) [†] ∪48987	038987 arabidopsis
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3.6	4	1.7	602	< ₽87209	P87209 kluyveromy
3.7	وا	1.7	671	< Q96W17	Q96wi7 trichoderma
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ALIGNMENTS

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RΑ
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ΚN
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PΓ
12 T
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1.44
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                                           TO PHEARMINGTESSWAQNEDEROREDE DEBERVORTERDITEDAVIOLERTEDOSVSS (1)
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130
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( ) X
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    pates A.C., Wilks A.F.;
     "How many PTKs to organise a worm?";
     The Worm Breeders Gazette 14:87 87(1995).
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RD
    Dates A.C., Wollberg P., Achen M.G., Wilks A.F.;
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RΑ
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"Functional annotation of a full-length mouse cDNA collection.";
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01-DEC-2001 (TrEMBLrel 19, tast annotation update)
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ΟX
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RT.
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         Ephydreidea: Prezephilidae: Drosophila.
NCB:_taxID=7027;
cva
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ΉN
RΡ
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          SIRAIN BERRELEY;
RX
          MEDLINE 20196000; PubMed 10731132;
         Adams M.D., Schulker S.E., Holt K.A., Evans S.A., locayne J.D.,
TO A
          Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
         George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
         Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
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         Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
         Abril J.F., Aqbayani A., An H.-J., Andrews:Ptannkoch C., Baldwin D.,
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Cherry J.M., Cayley F., Dahlke C., Davenport J. P., Davies P.,
de Pablos B., Deicher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
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Fin
         Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
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EΑ
KA
          Reinert K., Remington K., Saunders R.D.C., Schooler F., Shen H.,
          Shue B.C., Siden-Klames L., Simpson M., Skupski M.P., Smith T.,
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RA
          Wang E. Y., Wassarman D.A., Weinstock C.M., Weissenbach J.,
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Ye J., Yeh E. F., Kieri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
Zheng X.H., Zhang P.N., Zhong W., Zhou X., Zhu X., Smith H.O.
F.A.
12.0
          Gibbs R.A., Myst. S.W., Rubin C.M., Venter J.C.
           "The genome separate of Drosophila melanogaster."
RT
          Datence 287.2185 2195(2000).
KL.
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RP
          SEQUENCE FROM N.A.
          STRAIN DREGON-R;
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         STRAIN-OREGON R;
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RP
         SEQUENCE FROM N.A.
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SEQUENCE OF 14: 582 FROM N.A.
     STRAIN BERKELEY:
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     Robin 1 M., Wan K.H., Harvey 1., Lewis S.E., Brokstein P., Isang G.,
     Aubayers A. Arcsina L.L., Easter E., Plazej Ind., Jutenhett d.,
      Stamp Mo. Shaver Mo. Bow Mo. Beyle C.M., Farran D.E., Frige E.,
     Salle R., George R.A., Harris N.L., Hoskins P.A., Evans Heim M.,
     Heust n K.A., Hummarti S.R., Kim E., Li P., Morshreti M., Pacleb J.M.,
     Park T., Sepherra A., Sethi H., Shir E., Svirskas P.R., Weinburg T.,
     Children of the
     "Full Length Drosophila melanogaster cDNA pequence.",
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     Submirited (AUG 1999) to the EMBG/75 hWhite,700 Ed databasees.
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      I SUMPLARIOUS BUILDINGS IN THE SER, MUS FAMILY IN PRITEIN KINAMEN.
     EMBL. Alcostro: AAF45614.1; ...
     EMBL: AF020 (10: AAB71398.1)
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     EMBL: AF020:009; AAB71397.1;
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     EMBL: AE181(49) AAD55435.1;
     HSSP: 25.3450; IA05;
     ElyBale: FBun0023169; SNEIA.
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     interiors Tikovo'les Kuk pkinise.
     Interpro: Likouzz90; Ser thr pkinase
     Fram; closer; pkinase; 1.
      SMART SMOOLED; B TKe; I.
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     FROSILE, PSC (108) PROTEIN KINASE SI; 1.
     Air I share Serine, "The time probable former, true, terms."
     DEGOED 1 182 AA; 54500 MW. BD6804E308278BCB CR064;
  Emirita Marial.
                           -1.98; Stone 10; (dk 5) Length 582;
  Book Local Similarity Toology Fred, No. 0,14;
  Multibos I: Conservative of Mismatches () Indels () Caps (9)
      The EVKIAGE DECISE.
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                 CRELIMINARY:
                                   AA B'S STREET
     PHV RQF
     of MAY 2000 (TrEMBErel, 13, Crested)
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     PULATIVE TAKE PROTEIN (CG) 388 PROTEIN) (DD42274F).
id:
     MAKE OF STEENS OR COLBAND.
     Drosophila melanogaster (Fruit fly).
     Takiry ta: Metazoa: Arthropoda: Iracheata: Hexapoda: Insecta:
     Pteryosta: Neoptera: Endopteryqota: Diptera: Brachycera: Muscomorpha,
     Prhydr :dea: Prosophilidae: Drosophila.
+X
     NOBLITICALD 7.27:
1712
     SECUENCE FROM N.A.
     JURAIN OF KREETY,
     MEDILINE 20196506; PubMed 10731132:
     Atms Mit., Celniker S.E., Holt R.A., Evans C.A., Godayne J.D.,
     Amanati fes 2 %, Scherer S.E., fi P.W., Hoskins R.A., Galle R.E.,
     Scharge R.A., Sewis S.E., Richards S., Ashburner M., Henderson S.N.,
     Button 1.1. Wortsen J.R., Yandell M.E., Zhang Q., Chen L.X.,
Brandon E.C., Rogers Y. H.C., Blazej R.C., Champe M., Pfeiffer R.D.,
     Was Kir Doyle to Baxter Hid., Helt G., Nelson C.R., Miklos G.L.G.,
     Abrill 1887, Adbayani A., An H. J., Andrews Pfannkoch C., Baldwin D.,
     Pallew M.M., Bush A., Baxendale J., Bayraktaroqin L., Beasley E.M.,
     Beeson F.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
     Birkovilli, Bitchan M.R., Bouck J., Brokstein P., Brottier P.,
    Firtis f.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
     Sherry M., Tawley S., Dahike S., Davenport E.B., Davies P., de Labi s B., Delcher A., Deng Z., Mays A.D., Dew L., Dietz S.M.,
     To taon to Thomps L.E., Downes M., Dustan Rocha S., Dunkey R.C., Daran P.,
     Barbin & C., Campelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
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RA Fosler C., Gabrielian A.E., Garq N.S., Gelbart W.M., Glasser K.,
    Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
    Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
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    Rimms i P.E., Keiling the Frank to Kravite for Emily D., Lai Z.,
Lasko P., Loi V., Jovitsky A.A., Li J., Li Z., Liana Y., Lin X.,
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    Pulannolo M., Pittman G.S., Pan S., Pollard J., Pari V., Reese M.G.,
    Fringet E., Femiliaton F., Maunders R.D.C., Ochecler P., Shen H.,
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    Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
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     Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
     Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
     Theng X.H., Thong P.N., Thong W., Thou X., The E., The X., Smith H.e.,
     Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
     "The genome sequence of Drosophila melanogaster."
     Science 287:2185-2195(2000).
RN
     121
     SPOHENCE FROM N A
1/12
     Takatsu Y., Nakamara M., Stapleton M., Danes M., Matsumoto M.,
     O'Connor M.B., Shibuya H., Ueno N.;
                   o troogía o Hás Pimer, Maleana, mis coltan abas esc
     Pubmitted ( )
     SEQUENCE FROM N.A.
14.54
     STRAIN Y, ON BW SP:
     Stapleton M., Brokstein P., Hond L., Agbayani A., Carison J.,
     Champe M., Chavez C., Dorsett V., Partan D. Frise E., George R.,
     Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J.,
     Numboo J., Pacleb J., Paragas V., Park S., Phomanenavong S., Wan K.,
     Yu C., Lewis S.E., Rubin G.M., Celniker S.;
     Submitted (AUG 2001) to the EMBL/GenBank/DDBJ databases
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    EMBL; AE003571; AAF50895.1; .
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     InterPro: IPR001990: Granin.
     InterPro; IPR002290; Ser_thr_pkinase.
     InterPro: IPR004040; STY pkinase.
     InterPro; IPR001245; Tyr_pkinase.
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     PROSITE: PS50011: PROTEIN_KINASE_DOM: 1.
Ð₽
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     Serineythreonine protein kinase: Transferase
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      220 WEVLSRKOPF 229
          TELLIBER
      204 WEVLSRKOPF 21+
RESULI 7
090XC2
10 990802
                 PRELIMINARY;
                                   PRI; 697 AA.
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     01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DT
     NIMA-RELATED KINASE 8.
DE:
CN
     NEK8.
     Brachydanio rerio (Ecbratish) (Ecbra dario).
OS
     Bukary: ta: Metadoa; Churdata; Cramiata; Vertebrata, Euteleostomi,
000
-oc
     Actinopterygii; Neopterygii, Teleostei, Euteleostei, Ostariophysi,
     Cyprinitormes: Cyprinidae: Danio.
OC
     NCRI_TaxID=7955;
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ŔΝ
     E1.1
RP
     SEQUENCE FROM N.A.
RΑ
     Liu S., Lu W., Obara-Ishihara T., Drummond I., Beier D.R.:
     "A detect in a novel Nek-family kinase causes systic disease in the
     mouse and in zebrafish.";
Schmitter (AUC 2001) to the FMRI CenPark ODP L databases
     EMBL; AF407580; AAL09676.1; .
DR
ΚW
     Kinase.
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SO
                           1 9%: Score 10; DR 13; Length 697;
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      146 DEKTONTELD 155
          TELLIFIER
Db
      128 DEKTONILED 137
RESULT 8
0912R4
TD 091284
                                    PRT; 698 AA
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    0912R4:
DT
     01-DEC-2001 (TrEMBLrel. 19, Created)
     01-DEC-2001 (TIFMPI of 15, Erst sequence update)
01-DEC-2001 (TIFMPI of 15, East sequence update)
NIMA-RELATED KINASE 8
DT
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GN
     NEK8.
     Mus muscrifus (Mouse).
Eukaryota: Metazea: Cherdata; Craniata; Vertebrata; Euteleostomi,
OC.
CC
     Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
\bigcirc X
     NCBI_TaxID 10090;
     [1]
     SEQUENCE FROM N.A. STRAIN-057BLZ6J;
RP.
RC.
     Liu S., Lu W., Obara-Ishihara T., Drummond I., Beier D.R.;
     "A dotect in a new Littlek facili, kinase lanses cystle disease in the
     mouse and in zebratish.";
RL.
     Submitted (AJG-2001) to the EMBL/GenBank/DDBJ databases.
DR
     EMBL: AF407579; AAL09675.1; -.
KW
     Kinaso
     SEQUENCE: 698 AA; 75264 MW. 686B29A8C 180E94 CRC64,
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      146 DEKTONELED 155
         - 114:3314113
      128 DLKTQNILLD 137
RESULT 9
U9GJS5
ID 09GJS5
                  ∂RELIMINARY:
                                    PRT:
                                             22 AA.
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AC.
    01-MAR-2001 (TrEMBLrel. 16, Created)
DT
     01-MAR-2001 (TrEMBLrel, 16, Last sequence update)
DT
     01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
     CA2+/CALMODE IN-DEPENDENT KINASE (FRAGMENT).
DE:
     Lagenorhynchus obliquidens (Pacific white-sided dolphin).
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Eukaryota; Metazoa; Thordata; Craniata; Vertebrata; Euteleostomi;
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OC
    Lagenor hynchus.
    NCBI_TaxID-90247
RN
    1.1
RF
    SEQUENCE FROM N.A.
    STRAIN LOB_143_B, AND LOB_143;
Hare M.F., Cipriano F., Palumbi S.R.;
RC.
     "Slow Evolution of Genetic Monophyly in Delphins: Implications for
    Speciation, Systematics and Conservation.":
    Submitted (APP 1999) to the FMBL/CenBank/ODB! databases.
     EMBL: AF140810: AAF98663.1: -.
DR
     EMBL; AF140809; AAF98662.1; ...
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    Kinaso
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     NON_TER
     Mortal Land
    GEQUENCE 22 AA, 2346 MW. AZA16ACBDAF (BDDC CRC64)
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  Best Local Similarity 100.0%; Pred. No. 0.09;
  Matches 9; Conservative 0, Mismatches 0: Indels 0: Gaps
      161 KIADFGLSK 169
         11111111
Db
       8 KIADEGLSK 16
RESULT 10
O9GJWD
LD 09GJW0
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                                 PRT: HEAA
    09G.IW0 :
    01:MAR:2001 (TrEMBLref. 16, Created)
    01-MAR-2001 (TrEMBLrel, 16, Last sequence update)
    01 JUN 2001 (TrEMBLiel, 17, Last annotation update)
    MADE, MALMODULIN DEFENDANC KINASE (FRAGMENT).
     Lagemorhynchus obscurus (dusky dolphin).
     Pukaryota; Metazoa; Chordata; Craniata; Vertebrata; Futeleostomi;
     Mammalia; Eutheria; Cetartiodactyla; Cetacea; Odontoceti; Delphinidae;
     Lagenorhynchus.
\bigcirc x
    NCBI TaxID: 27611;
RN
    RP
     SEQUENCE FROM N.A.
    STRAIN-VARIOUS STRAINS:
     Hare M.P., Cipriano F., Parambi S.R.;
     "Slow Evolution of Genetic Monophyly in Dolphins: Implications for
    Speciation, Systematics and Conservation.";
     without the Light the two, Sankard, Maket databases.
     EMBL; AF140820; AAF98673.1;
    EMBL; AF140813; AAF98666.1;
     EMBL; AF140814; AAF98667.1;
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    EMBL; AP140817; AAF98670.1;
DR
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     EMBL: AF140819: AAF98672.1: -
     InterPro: IPR000719; Euk.pkinase
    Pfam; PF00069; pkinase;
     PROSITE; PS50011; PROTEIN KINASE DOM; 1.
    ATP binding, Kinase: Transferase.
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\Gamma^{*}\Gamma
    NON_111k
                         + 4
    SEQUENCE 33 AA: 3604 MW; 0604A909F35C0E01 CRC64;
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                                                                0: Gaps
      161 KIADFGLSK 169
       19 KTADEGLSK 27
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   Ç +(17V9);
    Tel MAR Let L (unEMBGrell, 16, Created).
    0. MAR . 01 (TrEMBEROL. 16. Last sequence update)
     -d ON . of (FrEMBErel, 17, Last annotation update).
    PARTAMENDULEN DEPENDENT KINASI, (PRAGMENT).
    Latemorfspachus abliquidens (Pacific white sided dolphin).
     Easkaryota: Metazoa: Chordata; Standata: Vertebrata; Eutéleostomi;
     Mammali. Butherra: Cetartrodactyla: Cetacea: odomtoceti: Delphimidae:
     discussion type thus
     NOBE TaxII: 90.47;
17 N
     SHOURING: EROM N.A.
     SUPAIN . OF 11 1 B. LOW 1137, DOR 1405, AND LOW_1477;
     Hate M.E., Cipriano F., Palumbi S.R.;
     "Goow E duties of Genetic Monophyly in Dolphins: Implications for
     Speciation, Systematics and Conservation.";
     Submitted (After 1999) to the PMED Stenkink Spirit first river
     EMBL: A: 14080r: AAF98659.1; ...
     EMBL: A-14080 - AAP98656.1:
     EMBL: A: 140801: AAP98657.1;
     EMBCL: A-119801. AAF98658.1;
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    InterProc IPRC00719; Euk pkinase
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    THE STITE (1950 11) PROTEIN KINASE (2011)
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    All bibling, kinase, transferase.
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NON TEN 13
    SEQUENC: (CAA) GOD4 MW; DE04A909F3560E01 CRC64;
                           1.7%: Seere of DB 6; Length 34;
 Best Local Similarity (100,0%) Prod. No. 0.13;
  Matches 9; Conservative 0; Mismatches 0; Indels
      201 KINDOUGE INC
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        Or Klastif Hate at
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                P. LILIMINARY,
                                  PRI. VE AA.
    -gre1.7V8;
    Of MAR 2001 (FrEMBLief, 16, Created)
    191 MAR 2006 (TrEMBLiel, 16, Last sequence update)
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    CALE/ON MEDDELEN PERFOREUNE KINAGE (FRAGMENT).
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     Mammalra; Euthoria; Cetarfiodastyla; Cetacea; Odonfoceti; Delphinidae;
     It agenor synchus
     NORTH TELLS SEC. 17.
3. 51
     SUBJUENCY FROM N.A.
     STEATN LOB 1299 B. AND LOB 1289;
    Bare M.S., Cipriano E., Palumbi S.R.,
     "Trow for Justica of Genetic Monophyly in Dolphins: Implications for
     Special on, Statematics and Conservation."
     Submitted (APR Teer) to the EMBL/GenBank/DDBJ databases.
    EMBL: A: 140800, AAF98651.1:
i P
    EMBC,; A: 14080 1; AAE98660, L;
    InterPr : IPR 90719; Euk pkimake.
    THE STILL ESSENTIAL PROTEIN KINASE DOM: 1
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    N N LEE
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     NON LEE
              ** AA; $501 MW; $501E854# $500E01 CRC64;
     SHOUSENCE
                           (1) 74; Source by 198 by Length (3);
 Hest Losa, Similarity 100,0%: Fred, No. 0,13:
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9; Conservative 0; Mismatches 0; Indels 0; Gaps
      161 KTADEGLSK 169
          11111111
       19 KIADPOLSK 27
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Q9GJV7
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     Lagenorhynchus obscurus (dusky dolphin).
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\cap X
RN
     SEQUENCE FROM N.A.
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     "Slow Evolution of Genetic Monophyly in Dolphins: Implications for
     Speciation, Systematics and Conservation.";
     Submitted (AFK 1999) to the EMBL/SenBank/DDBS databases.
     EMBL; AF140816; AAF98669.1; -.
     EMBL; AF140815; AAF98668.1;
     InterPro; IPR000719; Euk pkinase.
     PROSITE; PS50011; PROTEIN_KINASE DOM; 1.
     AIP binding: Kinase; Transferase.
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     NON LER
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                 3 3
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     NON TER
                         4.4
     SEQUENCE 33 AA; 3598 MW; 0611FD1CA75C0E01 CRC64;
                          1.7%; Score 9; DB 6; Length 33:
  Best Local Similarity 100.0%; Pred. No. 0.13;
  Matches 9; Conservative 0; Mismatches 0; Indels
                                                                0; Caps
      161 KIADFGLSK 169
          1:11:1:1:1
Dit.
       19 KIADFGLSK 27
RESULT 14
⊖9GMH4
то ужини
                FREELIMINARY;
                                  PRI:
                                          H AA
     Q9GMH4;
DTC
    01-MAR 2001 (TrEMBLrel, 16, Created)
    -01:MAR-2001 (TrEMBLrel, 16, Last sequence update)
     01 DEC-2001 (TrEMBLiel, 19, Last annotation update)
     PAZ ZOALMODULIN DEPENDENT KINASE (PRAGMENT).
     Lagenorhynchus acutus (Atlantic white-sided dolphin)
     Eukarvota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
1.161
     Mammalia; Eutheria; Cetartiodactyla; Cetacea; Odonfoceti; Delphinidae;
     Lagenorhynchus.
^{\prime}
    NCBI Tax1D:90246;
ΗN
     i 1 1
     GEOGENCE PROM N.A.
     STRAIN LAC_9300;
     MEDLINE 20051255; PubMed 10583838;
    Hare M.P., Palambi S.R.;
     "The accuracy of heterozygous base calling from diploid sequence and
     resolution of haplotypes using allele specific sequencing.
RT
RT.
     Mol. Ecol. 8:1750-1752(1999).
     EMBL; AF140821; AAF98674.1;
     InterPro: IPR000719; Euk_pkinase
    Pram; PF00069; pkinase; 1.
    PROBLED PS50011: PROTEIN_KINASE_DOM: 1.
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    ATP binding; Kinase; Transferase.
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NON_TER 33 33
SEQUENCE 33 AA; 3604 MW; 0604A909F3500E01 CRC64;
  Query Match
                         1.7%; Score 9; E3 6; Length 33;
  Best Local Similarity 100.0%; Pred. No. 1.13;
  Matches +: Conservative 0: Mismatches 0: Indels 0: Gaps 0:
     161 KIADEGLSK 169
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       19 KIADFGLSK 27
RESULT 15
บุ 38987
ID Q38987
                PRELIMINARY;
                                  PRI; 55 AA.
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DT
    01:NOV-1996 (TrEMBLrel, 01, Created)
    01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
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    01-DEC 2001 (TrEMBLrel. 19, Last annotation update)
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    PROTEIN KINASE CATALYTIC DOMAIN (FRAGMENT).
    AK21.
\Box S
     Arabidopsis thaliana (Mouse-ear cress).
DC.
     Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
L)(*
     Spermatophyta; Magnoliophyta; eudicotyleions; core eudicots; Rosidae;
4.10
     eurosids II; Brassicales; Brassicaceae; Arabidopsis.
     NCB1_fax1D 3702;
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     SEQUENCE FROM N.A.
• RP
     STRAIN EIL O: TISSUE-LEAF;
кX
     MEDLINE 96123233; PubMed:8534852;
kΑ
     Thuemmler F., Kirchner M., Teuber R., Districh P.;
PΤ
     "Differential accumulation of the transcripts of 22 novel protein
\pm T
     kinase genes in Arabidopsis thaliana.";
     Plant Mol. Biol. 29:551-565(1995).
DR
     EMBL; X86966; CAA60529.1; -
     InterPro; IPR000719; Euk_pkinase.
DR
     Pfam; PF30069; pkinase; 1.
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DR
     PROSITE: PS50011; PROTEIN_KINASE_DOM: 1.
     ATP-binding; Kinase; Fransferase.
FT
     NON TER
     SEQUENCE 55 AA; 5910 MW; 0E55D6DBD25.A9FB CRC64;
 Query Match
                        1.7%; Score 9; 03 10; Length 55;
  Best focal Similarity 100.0%; Pred. No. ).2;
  Matches 9: Conservative 0: Mismatches 0: Indels 0: Gaps 0:
      160 VKIADEGLS 168
QY
         131 131
       13 VKIADFGLS 21
Db
Search completed: May 13, 2002, 21:37:13
Job time: 36% sec
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GenCore versica 1.5 Copyright (a) 1993 - 2000 - Compagen Ltd.

OM protein - protein search, using sw model

Run on: May 13, 2002, 21:30:00 ; Sharch time 33:25 Seconds

(without alignments)

628.829 Million cell updates/sec

Title: US-09-445-223-1

Perfect score: 540

1 MNGEAICSALPTIPYHKLAD.....PEILVVSRSPSLNLLQNKSM 540 Sequence:

Scoring table:

Gapop 60.0 , Gapext 60.0

105224 segs, 38719550 residues Searched:

Word size :

Total number of hits satisfying chesen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

SwissProt_40:* Database :

> Pred. No. is the number of results producted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result.		Query				
	Score		Length	DB	11)	Description
1		1 ?	448	1	APAB_CAVEC	g60475 mayia porce
2	7	1.7	469	1	KCC4 MOUSE	P08414 mus musculu
	· · ·	1.7	473	1	KCC4_HUMAN	Q16566 homo sapien
4	.,	1.7	473	1	KCC4_HOMAN KCC4_RAT	P13234 rattus norv
ė .	· · · · · · · · · · · · · · · · · · ·	1.7	512	1	KI10_ARATE	
4,	- J	1.7	576	1	SNF1_SCHFC	038997 arabidopsis
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ь в	,	1.7	619	1	SNF1 CANTE	900472 candida qla
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10	,	1.7	633	1	SNF1_CANAI SNF1_YEASI	P52497 candida alb
11		1.7	1100	,	JAES EA.	P06782 saccharomyc
12	· · ·	1.7	1124	1	JAK3_HUMA1	167.7. tailus
1.2	9	1.7		1	JAK3_MOUSI	P52333 homo sapien
14	8	1.5	74	1		062137 mus musculu 046383 chlorobium
15	8	1.5	98	1	CSMB_CHLT1	
16	8	1.5		î	FIXX_RHIMI AAK1_PIG	P09822 rhizobium m
17	8	1.5	174	1		Q09136 sus scrota
18	H	1.5	283	1	AAE1_HUMA1:	Q13131 homo sapien P70269 mus musculu
. o 19	٦	1.5	295 295	1	PKL1_MOUSE:	
2)	. н	1.5	311	1	KMLC_DICE	P25323 dictyosteli
21	8	1.5	342	1	CC23_TRYB :	P54666 trypanosoma
22	3	1.5	513	1	BMAP_HUMAT	Q9uk28 homo papien
23	8	1.5	518	1	DUNI_YEAG : AAK1 RAT	P39009 saccharomyc P54645 rattus norv
24	8	1.5	552	1	AAK2_HUMA 1	
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+ 1	8	1.5	661	1	Y537_HUMAN	P05130 drosophila 060285 homo suplem
32	H	1.5	842	1	PKL2_RAT	000285 Romo Sapien 008874 rattus norv
13	 ห	1.5	923	1	IOR DROME	
ر ب		1.3	923	-	11 P110.70.E	P18475 drosophila

+4	В	1.5	942	1	PKI.1_HUMAN	Q16512 homo sapien
35	3	1.5	946	1	PKL1_KAT	063133 rattus norv
16	8	1.5	980	1	CLV1_ARATH	ybsyd8 arabidopsis
37	8	1.5	984	1	PKT2_HUMAN	Q16513 homo sapien
3.8	H	1.5	999	1	RLK5_ARATH	P47735 arabidopsis
4 (g	8	1	1122	1	TIE2_MOUSE	Q02858 mus musculu
4 ()	ಕ	1.5	1.1 ± 4	1	TIE2_HUMAN	∪02763 homo sapien
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4.3	8	1.5	11.5	1	LIBI_BOVIN	QU6805 bos taurus
4.4	8	1.5	1.1.18	1	TIEL HOMAN	P35590 homo sapien
4.5	8	1.5	1196	1	ABL1_CAEEL	FO3949 caenorhabdi

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	A2AB_CAVPO STANDARD: PRI: 448 AA.
AC.	Q60475;
D.I.	01 NeV 1997 (Rel. 35. Created)
24	-01 NeW 1997 (Note: 15, East Mogaenho update)
) [16 OCT:2001 (Ref. 40, Last annotation update)
ÐΕ	Alpha 2B adremengic receptor (Alpha-2B adremoceptor).
IN	ABRA2B.
0.5	Cavia porcellus (duinca pig).
16	Eukaryòta; Motaccia; Chordatà; Cramiata; Vertebrata; Euteleostomi;
ж.	Mammalja; Eutheria; Rodentia; Hystricognathi, Caviidae; Cavia.
ìΥ	NCBI_TaxID=10141;
۲N	(1)
8P	SEOURNEE PROMINIA.
RC	STRAIN HARTLEY:
RX.	MEDLINE 96152574; PubMed 8573196;
кA	Svensson S.P., Bailey I.J., Porter A.C., Richman J.G., Regan J.W.;
RT	"Hoterologous expression of the cloned gained rig alpha 2A, alpha 2B,
रा	and alpha 20 maremoceptor subtypes. Radioligand binding and
₹T	functional coupling to a CAMP-responsive reporter gene.":
ζĹ.	Biochem. Pharmacol. 51:291 300(1996).
20	-! FUNCTION: ALCHA 2 ALKENERGIO RECEED RO MEDIATE THE CATEGERSAMINE-
10 10	INDUCED INHUBITION OF ADENYLATE CYCLASE HER CONTINUE ACTION OF G
	PROTEINS.
IC	-! SUBCELLULAR Location: Integral membrane protein.
10	*! SIMILARITY: BELONGS TO FAMILY 1 OF G PROTEIN COUPLED RECEPTORS.
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14.1	This SWISS PROCEEDING is copyright. It is produced through a collaboration
	between the Swiss Institute of Bioinformatics and the EMBL outstation
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30 30	the European Broinformatics Institute. There are no restrictions on it use by non-plotit institutions as long as its content is in no wo
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     " TNA legience and differential expression of the mouse."
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     "Throm somal localization of the human gene for brain-
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     sequence of a cDNA corresponding to a brain calmodulin binding
     Proc. Nat., Anad. Sci. U.S.A. 84:3038-3042(1987).
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DR
     EMBL; J03057; AAA37366.1; ...
     EMBL; X58995; CAA41741.1; .
DR
DR
     PIR; A29878; A29878.
    PIR: S17656; S17656.
DR
     HSSP; Q63450; IA06.
DR
     MGD; MGI:88258; Camk4.
     InterPro: IPR000719; Eak pkinase.
DR
     InterPro: IPR002290; Ser_thr_pkinase.
Like
    Ptam; PF00069; pkinase; l.
     SMART; SM00220; S fKc; 1.
    PROSITE; PS00107; PROTEIN_KINASE_AIP; 1.
    PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR
     PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
     Transferase: Serine/threonine-protein kinase; AIP binding:
    Calmodulin-binding; Alternative splicing.
                        469
PT
     CHAIN
                 306
                                  CALSPERMIN.
    DOMAIN
                 4.2
                        296
                                  PROTEIN KINASE
Pal
FΊ
     NE BIND
                  4 8
                         56
                                  AIP (BY SIMILARITY)
                         7.1
FΉ
     BINDING
                  7.1
                                  ATP (BY SIMILARITY)
                 16.0
                                  BY SIMILARITY.
PT
     ACT SITE
                        160
     DOMAIN
                 :18
                        337
                                  CALMODULIN BINDING (FOTENTIAL).
    CONFLICT
                 27B
                        280
                                  VLD -> CFG1 (IN REF. 2).
FΤ
                 ₹02
                                  N > T (IN REF. 2).
     CONFLECT
                        302
FT
    SEQUENCE
                469 AA; 52627 MW; CEIF98670822E975 CKC64:
  ouery Match
                           1.7%; Score 9; DB 1: Length 469;
  Best Local Similarity 100.0%; Pred. No. 0.37;
  Matches 9: Conservative 0: Mismatches 0: Indels 0: daps
      161 KTADEGLSK 169
          111111111
      178 KTADEGLSK 186
RESULT 3
KCC4 HUMAN
TO KCC4 HUMAN
                   STANDARD:
                                   PRT: 473 AA
    Q16566;
    01:NOV 1997 (Rel. 55, Created)
    01 NOV-1997 (Rel. 35, Last sequence update)
     16 OCT 2001 (Rel. 40, Last annotation update)
    catelum/calmodulin dependent protein kinase type IV catalytic chain
DIR
     (EST 2.7.1.123) ("AM kinabe-CR) (CaMK IV) [Contains: Calspermin].
DE
     CAMK4.
     Homo sapiens (Human).
OS
     Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Esteleostomi:
CIC:
     Mammalia; Entheria; Primates; Catarrhini; Hominidae; Homo.
\ominus X
     NCBI TaxID:9606;
     111
     SEQUENCE FROM N.A.
RD
     MEDILING 94375404; PubMed 8089075;
     Kitani I., ⊖kuno S., Fujisawa H.
     "cDNA - Loning and expression of human calmodalin dependent protein
R II
     kinuse IV.":
    J. Biochem, 115:637-640(1994).
RL.
    121
     SECRENCE PROM N.A.
RP
     TISSUE Cerebellum, and Thymus:
RC
    MEDITINE 94252566: PubMed 8194751;
     Bland M.M., Montoe R.S., Ohmstede C.A.;
     "The cDNA sequence and characterization of the
```

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- Ca2-Zealmodulin-dependent protein kinase Gr from human brain and
         Gene 142:191-197(1994).
RN
         SEQUENCE FROM N.A.
         TISSUE Blood;
RХ
         MEDLINE 94149862; PubMed 8107230;
RΑ
         Mosialos G., Hanissian S.H., Jawahar S., Vara L., Kieff E.,
         Chatila 1.A.;
          "A Ca2-7 about the dependent protein kinase, CaM kinase to, expressed
         after transformation of primary human P lymphocytes by Epstein Barrwirus (EMV) is induced by the EMV oncogo e LMP1.";
RΤ
         J. Virol. 68:1697-1705(1994).
cc
          -!- FUNCTION: CALSPERMIN IS A HEAT-STABLE, ACIDIC, CALMODULIN-BINDING
dd
dd
                PROTEIN.
         -!- CATALYTIC ACTIVITY: ATP + protein - ADP + O-phosphoprotein.
         -!- SUBCELLULAR LOCATION: SUBSTANTIAL LC 'ALIZATION IN CERTAIN NEURONAL
CC
                 NUCLE: (BY SIMILAPITY)
CC
         -!- ALTERNATIVE PRODUCTS: CALCIUM/CALMODITIN-DEPENDENT PROTEIN KINASE
CC
CC
                 TYPE IV CATALYTIC CHAIN AND CALSPERMIN ARE OBTAINED BY ALTERNATIVE
cc
                 SPLICING
cc
         -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC
                 CAMK SUBFAMILY.
CC
CC
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         or send an email to licensesisb-sib.ch).
CC
DR
         EMBL; DH0742; BAA06463.1; -
ЪR
         EMBL: 1.17000; AAA35639 1; -
DR
          EMBL; L24959: AAA18251.1; -.
         HSSP; ∪63450; 1A06.
DR
         MIM: 114080: -
DR
DR
          InterPro: IPR000719; Euk_pkinase.
         Pfam: PF00069; pkinaso; 1.
DF
DR
         SWAPI: AMOUNT STAKE I
DR
DR
         PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
         PROSITE, PS00108; PROTEIN_KINASE_SI; 1.
         prosting respect profits without from the reset with the first profits of the school profits because with the school profits b
DR
FW
        Calmodulin-binding: Alternative splicing
                                                         CALSPERMIN.
F"T
         CHAIN
                          310 473
46 300
         DOMATM
FT
                                                               PROTEIN KINKSE
                                52 60
FΤ
         NP_BIND
                                                               ATP (BY SIM LARITY).
FΙ
         BINDING
                                                               ATE (PY SIM LARITY).
                                                                BY SIMILARLY.
FT
         ACL SITE
                                164 164
F'T
         DOMAIN
                                322 341
                                                               CALMODULIN SINDING (POTENTIAL).
         SEQUENCE 473 AA; 51925 MW; EFEE51E56 2326DC CRC64;
                                                 1.7*; Score 9; D: 1; Length 473;
    Best Local Similarity 100.0%; Pred. No. 1.37;
                      90 Conservative O Mismatch t O Indels O cape
           161 KIADFGLSK 169
                   TT .3 L1 CT
           182 KIADEGLSK 190
RESULI 4
KCC4 RAI
                                    SIANDARD;
ID KCC4 kA1
                                                                  PRT: 474 AA
AC P13234;
DT
       01-JAN-1990 (Ref. 13, Created)
       01-APR-1993 (Rei. 25, Last sequence update)
       16-OCT-2001 (Rel. 40, Last annotation upcate)
        Calcium, almodulius dependent protein kinase type IV catalytis chain (80 2 7 t 12) (CAM kinase CB) (CAMK TV) (Contains, Calspermin).
DE
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Rattus norvegious (Rit).
     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
     Mammalia; Eutherla; Rodentia; Sciurognathi; Muridae: Murinae; Rattus.
     NCBI TaxID=10116:
ΗN
     [1]
KF.
     SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
     MEDITINE 91288548; PubMed 1648230;
     Ohmstede C.: A., Bland M.M., Merrill B.M., Sahyoun N.;
     "Belighthaship to panel one ding Tale/Calmodulin dependent protein kiname of and calsperming a gene within a gene.";
    Proc. Natl. Acad. Sci. U.S.A. 88:5784:5788(1991).
19.1
₩N
     SEQUENCE FROM N.A.
1711
     MEDILINE-91304-87; PubMed 1649-85;
     Means A.R., Cruzalequi F., Lemaqueresse B., Needleman D.S.,
     Slaughter G.R., Ono T.;
     "A movel California dependent pretein kinase and a male germ
     coll specific calmodalin-binding protoin are derived from the same
81
     deno
RL.
     Mol. Cell. Biol. 11:3960-3971(1991).
     [3]
     SEQUENCE OF 250-474 FROM N.A.
1810
     STRAIN-SPRAGUE-DAWLEY; TISSUE Brain:
    MEDILINE 89174617; PubMed 2538431;
     Ohmstede C.-A., Jenson K.F., Sahyoun N.:
     "Ca2//calmodulin dependent protein kinase enri hed in cerebellar
RT.
     gramule cells, identification of a novel neuronal
     calmodulin dependent protein kinase.";
FT
RN
     [4]
     SEQUENCE OF 306 474 FROM N.A., AND SEQUENCE OF 335-361.
КP
     STRAIN SPRAGUE - DAWLEY;
     MEDILINE 8912 (272) PubMed: 291489*;
     Ono I., Slaughter G.R., Cook R.G., Means A.R.:
     "Molecular cloning sequence and distribution of rat calspermin, a
     high attinity calmodulin-binding protein.";
     J. Biol. Chem. 264:2081-2087(1989).
      THE RIGHT WAS TAMED AS A DECEMBER AS EXPOSED FOR STREET KINASE.
(20)
         ENRICHED IN CEREBELLAR GRANULE CELLS.
      I BOWLEE WE CALLERELMEN IS A HEAT STABLE, ACTUAL, CALMOSTIN BUNCHNG
CC
CC
     -!- CATALYTIC ACTIVITY: AIP + protein - ADP + G-phosphoprotein.
! ALTERNATIVE FECTORS. TALTIUM/DAIM ORDER DESERVENT PROTEIN KINASE
         THE IN TALABETH HAIN AND TALSPERMIN AS DIADRED BY ALTERNATIVE
17/2
         SPLICING.
CC
      1 TISSUE SPECIFICITY, CALSPERMIN IS PREDOMINANTLY FOUND IN MAMMALIAN
('('
         TESTIS AND BRAIN.
(36
      I FIM. THE N TERMINAL OF CALSFERMIN IS BLOCKED.
      of Complanting and his is the sampling raming a a strain EIRASES.
cc
         CAME SUBFAMILY.
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     and the sample of the property of the same agreement (some both its possible with only become one
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    or send an email to license isb-sib.ch).
DR
    EMBL: M63334; AAA40865.1:
ÐΒ
    EMBL; M/4488; AAA40845.1; ALT_SEQ.
    EMBL; M64757; AAA40856.1;
     EMBL; M64757; AAA40817.1:
    EMBL: JU4600; AAA11867.1:
1:3k
     EMB1: "04446; AAA40990:1;
     PIR; A41103; TVRTC4.
DR
     HSSP; P00518; 1PHK.
     InterPro: IPR000719: Euk_pkinase.
DR
DR
     Interfac. IPR002250. Sei_thi_pkinase.
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Pfam; PF00069; pkinase; 1.

SMART, BMCCCCO, S_TEC; 1. FROUTER, PSOUTOT, PROTEIN_KINASE_AIP; 1.

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THE JULE PROVIDED PROJETY KINASE SEE THE
     PROBLEE, ESSOULT: PROTEIN KINASE DOM: 1.
     drumsterase, Scrine/Chromine protein kinase, All binding,
     Salabodu. A fundada lestas. Alternative spileing.
     THATN
                51.4
                       4.74
                                 CALSPERMIN.
    DE-MAIN
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                                 PROCEIN KINACE
                       296
     NE R ND
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                        1.4
                                 ALP (BY SIMILARLIY).
     BUNDONG
                        2.1
                                 ADE (BY SIMILARITY).
    ACT STILL
                       1600
                                 BY SIMILARITY.
                11.0
                       1.1.2
    DOMA: N
                                  CALMODULEN BINDING (FOIENTIAL).
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                       3.56.3
     DE MAIN
                                 THE LY MINE.
                4.3
                                 PHAY BLU.
    Lie MA N
     CONDLIC.
                4.1.
                       372
                                  T - M (IN REF. 2 AND 4).
     SEQUENCE
               -474 AA, 53133 MW; 56621A056440E023 08064;
  govern Mater
                          1.7%; Score 9; DB 1: Length 474;
  Best Local Similarity 100,0%; Fred. No. 0.37;
  Mat here is a servative so Mismatches so indels so daps
     THE KIASH Mate Time.
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      COMMITTED NAME OF
34 E00 014 T 15
KILD ARAIH
10 KITO ARATH STANDARD;
A1 208007; 2007; 001728;
                                 THREE SELECTION
     15 10L see (Ref. 38, Created)
     15 J.H. +++ (ich. 68, hast sequence aparte)
    St. MAR . W. 2 (Feel. 41, Last annotation update)
    SNET related protein kinese KINDS (EC.2.7.1. ) (AKINDO).
     KIND OF SKIND OR ATRODUSO OF 14P13.22.
    Arabidopsis traliana (Mouse ear cress).
     Eukaryo'a: Viridiplantae: Streptophyta: Embryophyta: Tracheophyta;
     Specimatophyta, Magnoliophyta; endicotyledons; core endicots; Rosidae;
    eurosid: [1]; Brassicales; Brassicaceae; Arabidopsis.
     NCBI Taxill: 37 2:
    141
    SEQUENCE FROM N.A.
ACC:
    MEDILINE > 3013 41, EqbMod 1339373,
     ie daen L., Ibemas M., Rianchi M., Halford N.C., Kreis M.:
     "Stracture and expression of a gene from Arabidopsis thaliana
     encoding a protein related to SNEL protein kinase.":
    otemen 1. (c.249 (1992))
    BIGGENCY FROM N.A.
1.1.
     STRAIN IV COLUMBIA;
     Lessard P., Kreis M., Thomas M.
     Paramitted (DEC 1996) to the EMBH/Stabbank/Stabbankes.
    SEQUENCE FROM N.A.
1-1-
     SCHAIN IV. CHOOMBIA:
    Middline 21016 20; PubMed 11130713;
    Basamousat M. Bemeke K., Rieger M., Ansorge W., Unseld M.,
    Firtman, B., Ville G., Bloecker H., Perez Alonso M., Obermaier B.,
    Decisiony M., Builtry M., drivell G.A., Mache R., Paladomenach P.,
    De Simone V., Thomshe N., Artiguenave F., Robert C., Brottier F.,
    Wincker F., Cattolico L., Weissenbach J., Saurin W., Quetier F.,
    Schaeter M., Maeller Auer S., Sabel C., Euchs M., Benes V.,
    Wormback E., Brzenek H., Erffe H., Jordan N., Bangert S.,
    Weedelmann E. Kranz H., Voss H., Holland R., Brandt P., Nyakatura G.,
RΑ
    -Verzi Λ., D'Asqelo M., Pallavicini A., Toppo S., Simionati B.,
     Somrad A., Hornischer K., Kauer G., Loehnert E. H., Nordsiek G.
I: A
    Reachest G., Charte M., Schoen et. Barques M., Lerol J., Climent J.,
    Navarro E., C Hado C., Perez Perez A., Ottenwaelder B., Duchemin D.,
     Cooke E., Laudre M., Berger Lliuro C., Purnelle B., Masuy D.,
    de Baar M., Miirse A.J., Alcaraz J. P., Coffet A., Casacuberta E.,
    Madort A., Artiriau A., Flores M., Liquori R., Vitale D.,
    Minimhaugt G., Haase D., Schoot H., Rudd S., Zaccaria P., Mewes H. W.,
    Mayer F.C.X., Kaul S., Iown C.D., Kee H.L., Pallon E.J., Jenkins J.,
    Roomey Ricco M., Walts A., Sterback I., Eujil C.Y., Shew T.P.,
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RA - Creasy T.H., Haas B., Maiti R., Wa D., Peterson J., Van Aken S.,
     Pai G., Militscher J., Sellers P., Gill J.E., Feldblyum T.V.
    Presss D., Lis X., Nierman W.C., Calzberg S.L., White O., Venter L.C.,
   Keaser (M., Kaneko I., Nakamura V., Sato S., Kato I., Asami'u E.,
Sasamoro S., Kimura I., Idosawa K., Kawashima K., Kishida Y.,
Kiyokawa C., Kohura M., Matsumoto M., Matsuno A., Maraki A.,
     Nakayama S., Nakazaki N., Shinpo S., Takeuchi C., Wada T.,
     - Walanabe A., Yamada M., Yasuda M., Tabata S.;
     "Sequence and analysis of chromosome 3 of the plant Arabidopsis
     thaliana.";
RL.
     Nature 408,820 822(2000).
I√ N
     SEQUENCE OF 1 19 FROM N.A.
RP
     STRAIN-CV. COLUMBIA:
\mathbb{R}\mathbf{X}
     MEDLINE 95115691; PubMed 7816049;
     Te Guen L., Thomas M., Kreis M.;
     "Gene density and organization in a small region of the Arabidopsis
     thaliana genome.":
     Mol. Gen. Genet. 245:390-396(1994).
RT.
      I FUNCTION, MAY PLAY AN IMPORTANT ROLE IN A SIGNAL PRANSDUCTION
CC
         CASCADE REGULATING GENE EXPRESSION AND CARBOHYDRATE METABOLISM IN
(2)
         HIGHER PLANTS
      1 HISSUE SPECIFICALY, EXPRESSED IN ROOTS, SHOOTS AND DEAVES.
      IN SIMILARITY: BELONGS TO THE SEL/THE FAMILY OF PROTEIN KINASES
Cit
         SNF1 SUBFAMILY.
00
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     entities requires a license agreement (See http://www.ichemib.ch/announce/
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     or send an email to licensedisb sib.ch).
('('
     EMBL; M93023; AAA32736.1;
DR
     EMBL; X79707; CAA56146.1; -.
DR
     EMBL; AC008261; AAF26165.1; -.
     EMBL; X94757; CAA64384.1; .
DR
     HSSP; Q63450; LA06.
     Mendel; 14016; ARAth; 2326; mn 14016.
     Mendel: 12898; ARAth: 2098:1.
     InterPro: IPR000719, Euk pkinase.
     interPro; IPR001772; kAl.
     InterPro; IPR002290; Ser_thr_pkinase.
     InterPro; IPR001245; Tyr_pkinase.
     InterPro: IPR000449; UBA.
     Ptam; PF02149; KAL; 1.
    Pfam; PF00069; pkinase; 1.
    Plam; PF00627; UBA; 1.
     PRINTS; PRO0109; TYRKINASE.
     HMART, DMCGDDC, H_IKC; I.
     SMART; SM00165; UBA; 1.
     PROSITE: PS00107: PROTEIN KINASE ATP: 1.
DR
    PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
    PROSILE: PS50011; PROTEIN KINASE DOM; 1.
    -fransferase; Serine/threonine-protein kinase; AIP binding;
     Phosphorylation.
     DOMAIN
                                   PRODUCED KINASE
1111
                 1.74
}"I"
     NP BIND
                  25
                        + +
                                   ATP (BY SIMILARITY).
FΤ
     BINDING
                  4 8
                         4.8
                                   ATP (BY SIMILARITY).
                 142
PT
     ACT SITE
                        142
                                   BY SIMILARITY.
                 175
                        175
                                   PHOSPHORYLATION (AUL: ) (BY SIMILARITY)
     MOD RES
    SEQUENCE 512 AA; 58373 MW; 5A18655A0AA505DF ('RC64;
  Query Match
                            1.7%; Score 9; DB 1; Length 512;
  Best Local Similarity 100.0%; Fred. No. 0.4;
  Matches 9; Conservative 0; Mismatches 0; Indels 0; Caps 0;
      160 VKIADEGLS 168
          11111111
      156 VKIADEGLS 164
```

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RESULT 6
SNF1_SCHPO
      SNF1_SCHPO STANDARD;
                                                                         PRT; 571 AA.
          074536;
          15-JUL-1999 (kel. 38, Created)
          15-JUL-1999 (Rel. 38, Last sequence update)
DT
DT
          15-JUL-1999 (Rel. 38, Last annotation update)
          SNP1 like protein kinase (BC 2.7.1. ).
          SPCC74.03C
          Schizosaccharomyces pombe (Pission yeast).
118
          Bukaryeta: Fuedi: Arbony: ta, Schim zatcharizyete...
Onlin saboharnay:etales, Schimsaschari;yetalese.
          Schizosaccharomyces.
\ominus X
          NCBI_laxID 4896;
          SEQUENCE FROM N.A.
RO
          STRAIN-972;
PA
          Morphy L., Harris D., Lyne M., Rajandream M.A., Barrell B.G.,
Submitted (STD:1998) to the FMBL Cember: 1948) dividiases
          -!- SIMILARITY, BELONGS TO THE SER/THE FAMILY OF PROTEIN KINASES.
                  SNF1 SUBFAMILY.
CC
CC
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          or send an email to license lish-sib.ch).
          EMBL: ALORI543; CAA20833 I; -
DR
          HSSP: P0 1518: 1FHK.
DR
          InterPro: IPR000719; Euk_pkinase.
          InterPro: IPR002290; Ser_thr_pkinase.
          InterPro: IPR000449; UBA.
DΒ
          Piam; PF00063; pkinase; 1.
         PRIGHT PROMOTE AND PROBLET PRO
          PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR
          Transferase; Serine/threonine-protein kinase; ATP-binding.
FT
                                     34 285
40 48
                                                                    PROTEIN KINASE.
          DOMAIN
          NP_BIND
                                                                       ATP (BY SIMILARITY).
F.T.
                                    4.0
FΤ
          BINDING
                                  63 63
156 156
                                                                       ATP (BY SIM LARITY).
          ACT_SITE
                                                                     BY SÎMILARI Y.
          SECUENCE 576 AA: 65996 MW: E5857E8F1/1F7B50 CPC64;
                                                     1.7%; Score 9; D3 1; Length 576;
     Best Local Similarity 100.0%; Pred. No. 1.45;
     Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps
             160 VKIM FOLD 168
                    111 (14
             170 VKIADEGLS 178
RESULT 7
SNF1_CANGA
         SMET CANCA
                                    STANDARD.
                                                                        TRI. 61 AA.
          000372;
          01-NoV 1997 (Rel. 35, Created)
          01-NoV 1997 (Ref. 35, Last sequence update) 15-JUL-1999 (Ref. 38, Last annotation update)
DE:
          Carbon catabolite derepressing protein k mase (EC 2.7.1.).
GN
          SMP1.
           Candida qlabrata (Yeast) (Torulopsis glabrata).
US
          Bullery to, Progr. As somy site, Sancherom, office, Saintheromycotes, Saintheromy office, illusporter saucheromy office, Candida. MCP1_Tav10-5478;
( ) Y
          [1]
          SEQUENCE FROM N.A.
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RC STRAIN-NCCLS84;
     MEDITINE 97101049: EmbMed 8945576;
     Petter R., Kwon Shang K.J.;
     "Disruption of the SNF1 gene abolishes trebalose utilization in the
     pathogenic yeast Candida glabrata.";
     Infect. Immun. 64:5269-5273(1996)
     -!- FUNCTION: ESSENTIAL FOR RELEASE FROM CLUCOSE REPRESSION. II
         INTERACTS AND HAS PURCIFONAL RELATIONSHIP TO THE REGULATORY
         PROTEIN SNEW. COULD PROSIDERTLATES CAIR (BY SIMILARITY).
CC
     -15 SUBCELLULAR LOCATION: ASSOCIATED WITH THE NUCLEAR MEMBRANE (BY
      I DIMILARITY, BENEARY I THE FER, THE PAMILY OF PROTEIN KINASES.
         UNEL SUBSEMBLY.
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     modified and this statement is not removed. There by and for commorcial continues may be a little beautiful before one of
     or send an email to licenseriab sibachja
     EMBL; 1.78130; AAB48642.1; .
     HSSP: P00518: 2PHK.
DR
     InterPro; IPR000719; Euk pkinase.
     InterPro: IPRO02290; Ser thr_pkinase.
     Pfam; PF00069; pkinase; 1.
DR
    SMART; SMORZJC; S_IKC; 1.
PF THE ; FARTER AT THE FUNASF_ATP; 1.
PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
SE
     PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
     Trunsferase; Serine/Chreonine protein kinase; ATP binding;
     Phosphorylation; varbohydrate metabolism; Nuclear protein.
              6 17 POLY-RUS.
9 290 PROTEIN K
     DOMAIN
     DOMA LN
                                    THOTTEIN KINASE.
                                     AIR (BY SIMILARITY)
1....
     NE BIND
                  F183 F183
     BINDING
                                     AIF (BY SIMILARITY).
                 161 161
194 194
     ACT_DITE
                                    BY SIMILARITY.
                                   THE SHERYLANDER (AST - ) (BY SIMPLARITY).
1.3
    MCG istac
                - 611 AA; 70049 MW; 89E17812A4900CDU CRC64;
    SEQUENCE
 Query Match 1.7%; Score 9; DB 1; Length 611; Best Local Similarity 100.0%; Pred. No. 0.47;
  Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps
      160 VKTADEGLS 168
          175 VKIADEGLS 183
RESHLT 8
SNF1_CANTR
15 SNET CANTE
                   JIANDARE,
                                   PRT, 619 AA.
AC
     094168;
     15-JUL-1999 (Rel. 38, Created)
     15-JUL-1999 (Rel. 38, Last sequence update)
     15-JUL-1999 (Rel. 38, Last annotation update)
D1
     Carbon catabolite derepressing protein kinase (EC 2 7.1.-).
     Camdida tropicalis (Yeast).
     Eukaryota, Pungi, Ascomycota, Saccharomycotina, Saccharomycetes;
     Saccharomycetales, mitosporio Baccharomycetales; Candida.
     NCHI TaxID 5482:
RN
     111
     SEQUENCE FROM N.A.
     Kanai T., eqawa K., Weda M., Tanaka A.:
      "Genetic evaluation of the function of SNF1 in Candida tropicalis.";
     Submitted (MAR 1309) to the EMPL, Gentard, DDR: catabases.
      THE PROOF OF THE PROPERTY OF A PROPERTY OF THE PROPERTY OF T
          PROTEIN SNE4. COULD PHOSPHORYLATES CAT8 (BY SIMILARITY).
      1 DUBCELLULAR LAMATION, ADDAMIATED WITH THE NUCLEAR MEMBRANE (BY
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         one by non-protest institutions as long as its content is limited as
        modified and this statement is not removed. Usage by and for commercial
         centration requires a license agreement (see http://www.lib. 40 - 1/ans. no./
          or send in email to License tistes ib.ch).
         EMBG: ALC:4530 RAA (GR80.1, ...
         (M, \mathbb{A}, \mathbb{P}) = \mathbb{E} \{ \{ 1, 1, 2, 2, 1, \mathsf{APM} \}
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         ThromProc. IPRC00719; Euk pkinase.
         Threnhy (IPR) 2200; Ber thr pkinase.
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         SMART, .M. 9229. S. IKC. 1
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        THE STIFF INSCRIBE PROPERLY KINASE DOME IS
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        Transfer set Lerine/threenine protein kinase; Air binding;
         Phosphorylation; Carbohydrate metabolism; Nuclear protein
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        ACT SITE
                                                              BY SIMILARITY.
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                                                             THE SCHOKYLATION (AUTO ) (BY SIMILARITY).
        Mad REES
                             -615 AA: 7032 CMW. SESENTER RESESSED 7 CRC64;
         SEQUENCE
    Quietro Matici.
                                                 1.7%; Shore 9; DB 1; Length 619;
   Best Local Similarity 100,0%; Fred. No. 0.48;
    Matches 9: Conservative 0: Mismatches 0, Indels
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  NET CANAL
        SIANDARD:
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        100.0497 Carrotter
         of off spin (edit 34, Freshold)
         of NOV 1007 (Ref. 6. Last sequence update).
          3 MAY 1999 (sel. 39, East annotation update)
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          furbon satabosite derepressing protein kinase (EC 2.7.1. ).
         SINE
          Indida abicins (Yeast).
         Eukarysta, Fusqi; Ascomycota; Saccharomycotina; Saccharomycetes;
         San har suveet ness mitosporie Saccharomycetales; Candida.
         Note: Takib 54 9 c
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        1.1.1
         SHE ENCY PROM N.A.
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         GERAIN ALTO S. C4 Z R SEE.
         MEDILINE 0805 (*24) PubMed 9393775;
11 A
         abotter of Chang Yorks Kwon Churca K. L.:
         "A semi bomos (pour to Saccharomyces corevisiae SNET appears to be
         essents i for the viability of Candida albicans.":
         Tobest Temes 65:4909 4912(1967)
± N
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         SHOURING CORE A 5.20 FROM N.A.
         LIBAIN ALSO S. CH. / B. HILL
         ing there is Kwin Change Kill.
         Submitted (MAS 1996) to the SMEL, Scalinsk, 1949 fatabanes
           THE FUNCTION. ESSENTIAL FOR RELEASE FROM SECOND REPRESSION. II
                INSTRACTS AND HAS EUNCTIONAL RELATIONSHIP TO THE REGULATORY
                PR JEAN ENEX. COULD PHOSPHORYLATES CATE (BY SIMILARITY).
           CONTRACTOR OF THE STATE OF A SECTION OF THE SECTION
                SIMILARITY).
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     between the Swiss Institute of Bioinformatics, and the EMBL outstation.
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     modified and this statement is not removed. Usage by and for commercial static require a license rate out [186, 300 p.//www.id. 76, 5/minomace/
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    or send an email to license isb sib,ch).
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DR
     EMBL: 1.78129: AAB48643.1:
     EMBL; L39263; AAA92456.1; .
DR
     HSSP; P05132; ICTP.
     InterPro: IPROGO719: Euk pkinase.
Lik
DR
     InterPro; IPR002290; Ser_thr_pkinase.
     Ptam; PF00069; pkinase; 1.
     SMART; SM00220; S 1Kc: 1.
     PROSITE: PS00107; PROTEIN_KINASE ATP: 1.
    PROSITE: PS00108; PROTEIN_KINASE ST; 1.
     PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
κw
     Transferase; SerineZthreonine-protein kinase; AFP binding;
     Phosphorylation; Carbohydrate metabolism; Nuclear protein.
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                                  POLY HIS.
     DOMAIN
                  1.6
     TEOMATN
                  5, 4
                         305
                                  PROTEIN KINASE.
177
                         6.7
FT
     NP BIND
                  5.9
                                   ATP (BY SIMILARITY).
1/1
     BINDING
                  82
                         82
                                   ATP (BY SIMILARITY)
     ACT_SITE
                 175
                        1.75
                                  BY SIMILARITY.
F"T
     MOD_RES
                 208
                         208
                                   PHOSPHORYLATION (AUTO ) (BY SIMILARLLY)
     COMPLICE
                                  TO AR (IN REF. 2).
111
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                 228
                                   AGPEVDV SSVQKLMI (IN REF. 2)
177
     CONFLICT
                         234
     CONFILICA
                         255
                                   YVMLCORLETEDEE OMECTVVDYHOMISS (IN
FI
FT
                                   REF. 2).
F"T
    CONFLICT
                 187
                        387
                                   A \rightarrow R (IN REF. 2).
FTT
     CONFLICE
                 416
                        416
                                  R = A (IN REF. 2).
                                  S \rightarrow L (IN REF. 2).
                 4 9 4
                       4.44
FT
     CONFLICT
                620 AA; 70005 MW; 1806C652B5061D2B CRC64;
     SEQUENCE
  Query Match
                           -1.7%, Score 9, DE 1, Length 620;
  Best Local Similarity [100.0%; Pred. No. 0.48;
  Matches 9; Conservative 0; Mismatches 0; Inde4s 0; Gaps
      160 VKIADFGLS 168
         189 VKTADEGLS 197
RESULT 10
SNFl_YEAST
    SNFI_YEAST
                    STANDARD;
                                   PR1; 633 AA.
    P06782+
    01-JAN-1988 (Ref. 06, Created)
     01-JAN-1988 (Rel. 06, Last sequence update)
     15:JUL-1999 (Rel. 48, Last annotation update)
    Carbon catabolite derepressing protein kinase (EC 2.7.1. ).
     SNET OR CATT OR CCRI OR PASI4 OR GLC2 OR YDR477W OR D8635.20.
     Saccharomyces cerevisiae (Baker's yeast).
     Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
()(°
     Saccharomycetales; Saccharomycetaceae; Saccharomyces
\ominus X
     NCHI TaxID-4942;
RN
     [1]
     SEQUENCE FROM N.A.
RD
     MEDIINE 86289463; PubMed 3526554;
     Celenza J.L., Carlson M.;
     "A yeast gene that is essential for release from glucose repression
     encodes a protein kinase.";
RT
     Science 233.1175 1180(1986).
RM
     [2]
     SEQUENCE PROM N.A.
RE
     Dietrich F.S., Mulligan J., Allen E., Araujo R., Aviles E.,
    Berno A., Carpenter J., Chen E., Cherry J.M., Chung E., Dancan M.,
RA
    HunickerSmith S., Hyman R., Komp C., Lashkar, D., Lew H., Lin D.,
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Moresdale b., Nakahara K., Namath A., Gefner E., Oh C., Fetel F.X.,

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Roberts D., Schramm S., Schroeder M., Slogren T., Shroff N., Winant A., Yelton M., Botstein D., Bavil R.W.;
FA
      Submitted (and 1995) to the EMBL/Gentar /DDBT databases
      SEQUENCE OF 274 284, 528 539 AND 622 630, AND PROSTROKYLATION SITE.
RD
      Mitchelhill K.L., Stapleton D., Cao G., House C., Michell B.,
k Y
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      Katsis F., Witters L.A., Kemp B.E.;
      "Mammalian AMF-activated prefer kinash shares structural and functional nomology with the catalytic domain of yeast Onil protein
ph
RT
      J. Biol. Chem. 269:2361-2364/1994).
      -!- FUNITION: ESSENTIAL FOR RELEASE FROM GLUCOSE REPRESSION. IT
CC
          INTERACTS AND HAS FUNCTIONAL RELATIONSHIP TO THE REGULATORY
CC
          PROTEIN SNP4. INTERACTS ALSO WITH SIP1, SIP2 AND GAL83. COULD
          PHOSPHORYLATES CATS.
      -!- SUBCELLULAR LOCATION: ASSOCIATED WITH THE NUCLEAR MEMBRANE.
      -!- SIMILARITY: BELONGS TO THE SER/THE FAMILY OF PROTEIN KINASES.
CC
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      modified and this statement is not removed. Usage by and for commercial entities requires a linease argument. See http://www.isb.sib.bl/chem.no/
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      or send an email to license isb-sib.ch'.
- DR
      EMBL; M13971; AAA35058.1; -.
DR
      EMBL; U330°0; AAB64904.1; -.
DR
      PIR: A26030; A26030.
      HSSP: 063450; 1A06.
DΡ
      Sith Sinnigers SMP1
-DR
      InterPro; IPR000719; Euk_pkinase.
DR
      InterPro; !PR002290; Ser_thr_pkinase.
      Pfam; PF00069; pkinase; 1.
DR
      SMART: SM0022) S_TKC; 1.
PROSITE: PS00107; PROTEIN_KINASE_ATP; .
DE
Lik
DR
      PROSITE; PS00108; PROTEIN_KINASE_ST; 1
      PROSTIE: PS50011; PROIEIN_KINASE_DOM: .
Transferase: Serime/threonine protein :inase: ATP-binding:
KW
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      Phosphorylation: Carbohydrate metabolism; Nuclear protein.
                18 32 POLY-HIS.
55 306 PROTEIN KI
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      DOMAIN
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      DOMA I N
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                                    PROTEIN KINASE.
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      RINDING
                   84 84
177 177
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FΤ
      ACT_SITE
                  177
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FT.
      MOTO REST
                                    PHOSPHORY ATTEM (AUTO )
                 633 AA - 72045 MW - PS063565098604P3 0P064
      SECUENCE.
  Query Match 1.7%, Score 9, DB 1, Length 633; Best Local Similarity 100.0%; Prod. Nc. 0.49;
   Matches 9: Conservative 0: Mismatches 0: Indels
       160 VKIALECLS 168
           111111111
       191 VEIADEGLS 199
RESULT 11
JAK3_RAT
      JAK+ FAI
                     STANDARD;
                                      PRT; 1100 AA.
      Q63272;
      01 NOV-1997 (Rel. 35, Created)
T:T
      01-NoV 1997 (Rel. 35, Last sequence of date)
I \cap I
      16-001-2001 (Rel. 40, Last annotation update)
      Tyrneine protein kinase JAKI (E. 2.7. .112) (Janus kinase 3, (JAK 3).
DE
      JAK3.
GN
US
      Rattus norvegicus (Rat).
      Eukarvota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
      Mammalia: Eutheria: Redentia: Sciuroq.athi: Muridae: Marinae: Rattus.
      NCBI_laxID 10116;
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SEQUENCE FROM N.A.
     TISSUE Spleen;
КX
    MEDITINE 94191816, PubMed 814386-9
     Takahashi T., Shirasawa T.;
     "Molecular croming of lat JAK3, a movel member of the JAK family of
     protein tyronine kinases.";
     FEBS Lett. 342:124-,28(1994).
     I FUNCTION. TYROGENE KINAGE OF THE NON SPEEDS TYPE, INVOLVED IN
         THE INTERLEUKIN 2 AND INTERLEUKIN 4 SIGNALING PATHWAY.
         PHOSPHORYLATES STAIR, IRSL IRSL AND PIBK.
CC
     -!- CATALYTIC ACTIVITY: ATP + a protein tyrosine - ADP + protein
CC
        tyrosine phosphate.
     -!- SÚBCELLULAR LOCATION: WHOLLY INTRACELLULAR, POSSIBLY MEMBRANE
        ASSOCIATED (BY SIMILARITY).
CC
     -!- LISSUE SPECIFICITY: TRANSCRIBED IN A VARIETY OF TISSUES INCLUDING
        SPLEEN, LUNG, KIDNEY AND INTESTINE.
     -1- DOMAIN: POSSESSES TWO PHOSPHOIRANSFERASE DOMAINS. THE SECOND ONE
        PROBABLY CONTAINS THE CATALYTIC DOMAIN (BY SIMILARITY), WHILE THE
         PRESENCE OF SLIGHT DIFFERENCES SUGGEST A DIFFERENT ROLE FOR
ce
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        DOMAIN 1.
     -1- PIM: TYROSINE PHOSPHORYLATED IN RESPONSE (* 11-2 AND 11-4 (BY
        SIMILARITY).
      I COMPLANTA BELL NOW TO THE OVER AMOUNT FOR THIS EINAFEE. DAK
     SUBFAMILY
         COMMINARION OF NOATH, COOP, COMAIN,
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     use by non-profit institutions as long as its content is in no way
    modified and this statement is not removed. Usage by and for commercial
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    or send an emair to licensemisb-sib.ch).
DR
    EMBL; D28508; BAA05868.1; -.
    HOME; PILBER; LACW.
DR
    InterPro; IPkUduz99; Band_4.1.
     InterPro: IPRO00716; Euk_pkinase.
    InterPro: IPROJO980: SH2.
    InterPro: IPR001245; Tyr_pkinase.
    Plam; PP00069; pkinase; 2.
    SMART; SM00295; R41; 1.
     SMARI; SM00252; SH2; 1.
    SMART: SM00219; Tyrkh: 1.
PROCITE: PS00167: PROFICIN_KINASE_AIP: 1.
    PROSITE; PS00109, PROTEIN_KINASE_IYR; I.
    PROSTITE PSSCOIL PROFIN_KINASE_POM; 2.
PROSTE, PSSCOIL SEC. PALSE_NEG.
     Transferase: Tyrosine protein kinase: ATP-binding: Phosphorylation;
    SH2 domain; Repeat.
    in MAIN
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                                  SH2 (ATYPICAL).
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                                  PROTEEN KINASE 2.
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    NP BIND
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                                  ALP (BY SIMILARITY)
    BINDING
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    ACT_SITE
                                  BY SIMILARITY.
                 971
                       976
                                  PHOSPHORYLATION (AUTO) (BY SIMILARITY).
     MOD, RES
               1100 AA: 122560 MW: 1059CA05F4FD7EE, CRC64:
    SEQUENCE
                          1,7%; Score 9; DB 1; Lerath ilou;
 Query Match
  Best Local Similarity 100.0%; Pred. No. 0.83;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Saps 1;
      159 HVKIADEGL 167
         111111111
      of a HVKTADEGL See6
RESULT 12
JAK3_HUMAN
ID JAKK, HUMAN
                   STANDARD:
                                   PRI; 1124 AA
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A(*) - P<sup>1</sup> 23 (*) - Θ[ G.59) - Θ[ 3260] - Θ[ 30] [ 1)
     of odd Peeb (Rel. 34, Streated)
     of Oct. (Bt (Ref. CL. Last sequence apdate)
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    - 01 MAR 2002 (Rel. 41, Last annotation update)
     thromate protein kiname JAKA (MC 2.7.1.112) (Janus kiname A) (JAK A)
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     (Leuk ante lanus kinase) (L.JAK).
    -Benno Superens (Bonnan).
- Bukar - th. Methora, Moseluta, Transata, Vertebrata, Botela out mis
     Manumalar Estheria; Primates; Catarrhini; Hominidae; Homo.
     NOBL INTO HORSE
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     звойвал вком м.А. (празакм д).
Pit
1/ X
     MEDIJIAN 042 04304; IndoMed 80221 00;
     Kiwan di M. McVicar I.W., Johnston J.A., Blake F.E., Chen Y. Q.,
     Tal B K . Loyd A.R., Kelvin E.J., Stoples J.E., Ortaldo J.R.,
       Shear falls
     "Mode of it storing of a JAK, a James family protein tyrosine kinase
1. 1
     expressed in natural killer seals and activated leakocytes.",
47.1
     From: Natl. Acad. Sci. U.S.A. 91:6374-6378(1994).
PN
37.17
     SEQUENCE FROM N.A. (ISOFORMS I AND 3)
     MEDIANE 960 : Moder Impleed 755 on ck;
     sas K.S., Jon Y., Graham P.K., witthain B.A., Thie J.N., Liu E.I.,
     "A kirase deticient splice variant of the bases JAKS is expressed in
     hemat resets and epithelial cancer cells.";
     J. Bici. Chem. 270:25028-25036(1995).
RT.
RN
     SECUENCE OF BUILDING N.A.
1010
     MEDIATE: 162 1884%; PubMed 86627.18;
PX
     Verbsr; J.W. Bach E.A., Fang Y.E., Yang L., Randolph D.A.,
     Field, L.E.:
     "Emprove that it though kinds to all human endethellar and other non-tympheted and non-myeloid cells.":
     31 Bi 1. Chem. 271i13976 (3986(1996).
Ref.
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     VARIANC STHESTYS 100.
1011
     Madistrian of Residual Furners Technisms
     March, E., Viila A., Giliani S., Sacco M.S., Frattini A., Porta F.,
HΑ
     Markin A.J., Mohnston J.A., Candotti F., O'Shea J.J., Vezzoni P.,
     Notarangelo 1.b.;
     "Mota", and of take toponomia patients with autoromal severe combined
ИL
     commune deficiency (SCID).":
     Nature 517:6 - 68(1995).
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RD
     VARIANCE SCI. GLY 481; 585 LEU MET 592 DEL AND ARG 759.
     MEDILIN 1980, 793; Indomed 935450 8;
     'indot'ı F., Dakes S.A., Johnston J.A., Giliani S., Schumacher R.F.,
RΑ
     Mella Fi rini M., Uqazio A.G., Badolato R., Notarangelo L.D.,
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     Bootsi
             .. Marchi P., Strina D., Vezzoni P., Blaese R.M., O'Shea J.J.,
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     Villa 3
     "Structural and functional basis for JAK3 deficient severe combined
     communicated interiors, ";
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     15,00 d to 39 m 4003 (1997)
l- N
    1.6.1
     VARIAN LINE IPP 682.
10.65
     MEDILIN: 9842 (994) PubMed 97530725
     Rockies - Letting G., Villa A., Badolito R., Schumacher R.E.,
    Khalii J., Lorselet J., Brescrani S., O'Shea J.J., Vezzoni P.,
i. A
     Notara relection. Candotti E.,
     "Modec for and bischemical characterization of JAK3 deficiency in a
     gations with severe combined immunodeficiency over 20 years after
     tone more ow transplantations amplications for treatment.";
     Br. J. Saematol. 102:1363 4366(1998).
: N
     VARIANCE SCHE AND 151; THE 722 AND SER 910.
     MEDULINE 2013 054: PubMod 1698/185;
     i thoma ber kir., Mella P., Badolato k., Florini M., Savoldi G.,
11 A
     Stituans St. Veila A., Candotte F., Lampalini A., C'Shea J.J.,
     Nothing become and
     " Sample to genomic organization of the human JAK3 gene and metation
    countys. In revere combined immanded beloncy by single strand
    is automost one polymorphism.":
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Hum. Genet. 106:73 79(2000).
      I FUNCTION, TYROSINĖ KINASE OF THE NON RECEPTOR TYPE, INVOLVER IN
CC
         THE INTERLEGKIN 2 AND INTERLEGKIN 4 SIGNALING PAIHWAY.
         PHOSPHORYLATES STAIR, IRSL, IRSZ AND PICK.
      ! CATALYFIC ACTIVITY: ATP + a protein tyrosine - ALE + protein
CC
        tyrosine phosphate.
        SÜRCELLULAK LOCATION: WHOLLY INTRACELLULAR, HOSSIBLY MEMBRANE
(10
        ASSOCIATED (BY SIMILARITY).
      T. ALTERNATIVE PROTESTS: A Proference, LAMARGEAR ast JAKA.
         2, MARKER, Squite MARKER (shows here; and sy MARRM, Sattinated monosytes
etc.
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         JAK3; are produced by alternative splining, (soform 1 may be
CC
         defective as it lack some part of the kinase domain.
        TIGSUE SPECIFICATY: IN MK CELLS AND AN NK LIKE CELL LINE BU! NO!
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         IN RESIDENCE CONTROL OF IN STHER TESSUES, THE S FORM IS MORE
CC
         COMMONLY SEEN IN HEMATOPOLITIC LENES, WHEREAS THE B. AND M. FORMS
eje:
         ARE DETECTED IN CELLS BOTH OF HEMATOPOLETIC AND EPITHELIAL
CC
         ORIGINS.
        DOMAIN, PROSECUES INCOME OF CHARGE FRANCE FRANCE OF MAINS. THE SECOND ONE
         PROBABLY CONTAINS THE CATALYTIC DOMAIN (BY SIMILARITY), WHELE THE
CC
         PRESENCE OF SLIGHT DIFFERENCES SUGGEST A DIFFERENT ROLE FOR
CC
         DOMAIN 1
CC
      ! PTM: TYROSINE PHOSPHORYLATED IN RESPONSE TO IL-2 AND IL-4.
      * DISEASE: DEFECTS IN TAKE ARE A CAUSE OF RECESSIVE T-CELL
         NEGALIVEZE CELL POSITIVE SEVERE COMBINED IMMUNODEFICIENCY (I B)
CC
         SCID), A CONDITION CHARACTERIZED BY THE ABSENCE OF CIRCULATING
CC
         MATURE TELYMPHOCYTES AND NK CELLS, NORMAL TO ELEVATED NUMBERS OF
cc
         NONFUNCTIONAL B-LYMPHOCYTES, AND MARKED HYPOPLASIA OF LYMPHOIL
CC
         LISSHES
      ! SIMILARITY, BELONGS TO THE TYR FAMILY OF PROJEIN KINASES, JAK
CC
         SUBFAMILY.
CC
     -! SIMILARITY: CONTAINS I SH2 DOMAIN.
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    This CWISC PROT cutry is suppright. It is produced through a collaboration
    between the Swiss Institute of Bioinformatics and the EMBL outstation
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    the European Bioinformatics Institute. There are no restrictions on lits
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    or send an email to license isb sib.ch).
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    EMBL; U09607; AAA19626.1; ...
DR
    EMBL; UH1601; AAC60226.1;
1118
    EMBL; U31602; AAC50227.1; -.
     EMBL: U57096; AAC50542.1; ...
    HSSP; P11362; 1FGK.
DR
     MIM; 600173;
     MIM; 600802;
    InterPro; IPR000299; Band_4.1.
DR
     InterPro; IPRO00719; Euk_pkinase.
     InterPro; IPR000980; SH2.
DR
DR
     InterPro: IPR001245; Tyr_pkinase.
    Ptam; PF00069; pkinase; 2.
    SMART: SM00295: B41: 1.
DR
     SMART; SM00252; SH2; 1.
    SMART: SM00219: TyrKe: 1.
    PROSITE; PS00107; PROTEIN_KINASE_AIP; 1.
    PROSITE; PS00109; PROTEIN_KINASE TYR; 1.
    PROSITE; PS50011; PROTEIN_KINASE_DOM; 2.
    PROSITE; PS50001; SH2; FALSE_NEG.
     Fransterase; Tyrosine-protein kinase; AFP binding; Phosphorylation;
KW
    SH2 domain; Repeat; Alternative splicing; Disease mutation; SCID.
ΚW
    DOMATN.
                 375 475
                                  SH2 (ATYPICAL) .
    DOMAIN
                521
                       781
                                  PROTEIN KINASE I.
FT
    DOMAIN
                       1111
                                  PROTEIN KINASE 2.
PΤ
                822
    NP BIND
                                  ATP (BY SIMILARITY)
FΤ
                828
                       836
                855
    BINDING
                       REG
                                  ATP (BY SIMILARITY).
                949
FT
    ACT SILE
                        949
                                  BY SIMILARITY.
                                  PHOSPHORYLATION (AUTO ) (BY SIMILARITY).
FΤ
     MOD RES
                980
                       980
                                  HELMKLOWAPSPODRESESALOPOLOMEWSGSROCFTHAFT
ET
     VARSPLIC
                1071
                       1124
                                  AHPEGKHHSLSES - SAAGLASVSOSVDWAGVSGKPAGA
F E
                                  (IN ISOFORM I).
FΤ
    VARSPLEE
                1.371
                                  - ВЕНЬМКІ З'МАРОРО́ВЫ ОРОАЦ ЗЕДІЛИІ МООЗВОСТІ НАЕТ
FT
                     1424
                                  AHPECKHESLSES - SCYSCWRODICSMCWWPIVISRWI
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4.11
                                     LACSPORRELITATIVOLFFTLHATAASVAVENKTO (IN
FT
                                      ISOFORM 33
FT
     VARIANT
                                      Y - C (IN SCIDE.
                                     ZETIE-VAR 006284.
FT.
     VARIANT
                   151
                          15.1
                                      \hat{\mathbf{r}} = \mathbf{r} \cdot \mathbf{r} \cdot (\mathbf{IN} \cdot \mathbf{SCID}).
                                      ZETTA VAR 010492
F"I
                                     E \rightarrow G (IN 3C16)
F: L
     VARIANT
                   481
                          481
F: I
                                     /FIId VAR_010493.
F1
     VARIANT
                   582
                          582
                                     R -> W (IN SCID).
F.1
                                      ZETIG-VAR 010494
                                     MISSING (IN SCID, LACK OF PROSPHORYLATION
FT
     VARIANT
                   586
                          552
FT
                                     IN RESPONSE TO CYTOKINE STIMULATION;
34.1
                                      /FTId-VAR_010495.
FT
     VARIANI
                                     V I (IN SCIL).
ZETIG VAR_010496
FI
FΠ
     CHAINAV
                   759
                          754
                                        - - E (IN SCID, CONSTITUTIVE
F1
                                     PHOSPHORYLATION) .
FT
                                      /FT1d VAR_016497
                                     L \sim S (I\overline{N} \otimes CID).
FT
     VARIANT
                   310
                          910
FT
                                     /TT1d VAR_010498.
                                     A \rightarrow G (IN REF, 2).
FI
                  117
                                     MISSING (IN REF. 9).
FT
     CONFILING
                          147
                          197
Fi
     CONFILENT
                                     T A (IN SEF. t).
                          212
FT
     CONFLICE
                   212
                                     A \rightarrow R (IN \langle EF, 2 \rangle).
FT
     CONFIDE
                                     T - R (IN REF. 2).
                                     M -> 1 (IN REF. 2).
     CONFLICT
                  610
FΊ
     CONFLICT
                  845
                          846
                                     AH -> CD (I4 REF. 2).
                          897
     CONFILICI
                  H46
                                     PE -- QS (14 REF. 2)
                  1124 AA; 125015 MW; 100FD22368E088E4 CRC64;
-50
     SEQUENCE
                             1 7% - Socre un Oxito regish 1104
  Best Local Similarity 100.0%; Pred. No. ).84;
* Matches 9; Conservative 0; Mismatches 0; Indels
                                                                        0; Gaps
      159 HVKTADEGL 167
           1111111
      962 HVKTADEGL 970
RESULT 13
JAK3_MOUSE
    JAK3_MOUSE
                    STANDARD;
                                      PRT; 1299 AA
     Q62137; Q61747; Q61746;
     01-NoV-1997 (Rel. 35, Created)
DE
DT
     01-NOV-1997 (Rel. 35, Last sequence upda e)
1/1
     16-001-2001 (Rel 40, fast annotation update)
     Tyrosine profein kidase TAK3 (FC 2 7 1 1 2) (tanus kidase 3) (JAK-3).
GN
     JAK3.
OS
     Mus musculus (Mouse).
     Eukaryota: Metazoa: Chordata; Craniata; 'ertebrata; Euteleostomi;
     Mammalia Eutheria; Rodentia; Sciurografia; Muridae; Murinae; Mus.
...X
     NCRT_Lav'b-longo-
ИN
     SEQUENCE FROM N.A. (ISOFORM 1).
ED.
EX
     MELLINE 94309920; PubMed 7518579,
RA
     Rane S.G., Reddy E.P.;
RТ
      "JAK3: a novel JAK kinase associated wit: terminal differentiation of
RT
     hematopoietic cells.";
RT.
     Oncogene 9:2415-2423(1994).
RΝ
     SEQUENCE FROM N.A. (ISOFORM 2).
RP
     SIPAIN PAIP, M.X. 129 FT, fiscus Thymus, MEDLINE 96184772; Pubbmed 8605329;
PC.
EX
     Curniak C.P., Berg L.J.;
      "Murine JAK? is preferentially expressed in hematopoietic tissues and
     lymphocyte precursor cells.";
RI.
     Blood 87: 3151-3160(1996).
RN
     SEQUENCE FROM N.A. (180FORM 3).
     STRAIN BALLAT
     MEDITNE 94291024; PubMod 8022486;
КX
     Witthuhm B.A., Silvennoinen O., Miura O. Lai K.S., Cwik C., Liu E.T.,
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```
"formed-comment of the take? Same kinase is digusalling by interleakins
RT
         2 and 4 in Tymphoid and mycloid cells.";
        2 did a th lymphoto did mystere term.

Nature 370:153-177(1994).

FUNCTION. TYP-SINE KINAGE OF THE NON RECEIVED IVEE, INVOLVED IN
RT.
                THE INTERLEUKIN 2 AND INTERLEUKIN 4 SIGNALING PATHWAY.
               PHOSPHORYLAIRS STATE, IRSI, 1832 AND PLOK.
               CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
               tyrosine phosphate.
         -1- SUNCELLULAR LOCATION: WHOLLY INTRACFILLIAR, POSSIBLY MEMBRANE
CC
               ASSOCIATED (BY SIMILARITY).
               ALTERNALIVE (Red 00018) is (leaf-oRMS, I (lenewh nEkr), 2 AND 3; ARE
               TRODUCED BY ALTERNATIVE SPLICING.
               TISSUE SEES IN BUILTY. BIGHEST LEVELS FORMS IN THE THYMUS WITH
                SOMEWHAT LOWER LEVELS IN BONE MARROW, SPELISH, FRIAL LIVER AND
               ADULI CD4 CD8 THYMOCYTES. VERY LOW LEVELS IN ACOLI KIDNEY, LUNG,
                TECTES, BRAIN AND LIVER.
               DOMAIN. POLICEALLY INCOMESSMEDIKANSPEKASS DOMAINS. THE SECOND ONE
                PROBABLY CONTAINS THE CATALYTIC DOMAIN (BY SIMILARITY), WHILE THE
131
               FRESENCE OF SEAGHT DIFFERENCES SUGGEST À DIFFERENT ROLE FOR
CC
               FIRM, TYROJINE PROSPECKYLATED IN RESPONSE IN IL 2 AND IL-4.
               DIMILARITY, FEELINGS TO THE ITE FAMILY OF EXCHEIN KINASES, JAK
               SUBFAMILY.
               SIMILARITY, CONTAINS I SHE DOMAIN.
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CC
        or send an email to license isb sib.ch).
CC
DR
         EMBL; 1.43768; AAA21415.1; .
DR
        EMBL; L40172; AA-42085.1;
         EMBL; 1.32955; AAA21565.1; ...
DR
        HSSP; P11362; TAGW.
DR
DR
         MGD; MG1:99928; Juks.
        InterPro; IPROBUZ39; Band 4.1.
DR
        InterPro; IPR000719; Euk pkinase.
        InterPro; 1PR000980; SH2.
DR
        InterPro; IPR001.245; Tyr_pkinase.
TYR
        Plam; PF00069; pkinase; 3.
DR
DR
         SMAR1; SM00295; B41; 1.
        SMART; SM00252; SH2; 1.
       DR
        PROSITE; PS50011, PROTEIN KINASE DOM; 2.
        PROSITE; PS50001; SH2; FALSE NEG.
ΚW
         Transferase: Typesine protein kinase: ATP-bind.hg: Phosphorylation;
         SH2 domain; Repeat: Alternative splicing.
KW
                             5, (, ()
I'T
         DOMA UN
                                        6,803
                                                           SHZ (ATYPICAL).
INCHEIN KINASE 1.
                            732
        DOMATE.
                                         102
17
         DOMATN
                            1032
                                         1255
                                                           PROTEIN KINASE 2.
         NP_BIND
                            1038
                                        1046
                                                           ATP (BY SIMILARITY).
\operatorname{P}^{n}P
         BINDING
                            106.4
                                        106.4
                                                           ATP (BY SIMILARITY).
FΤ
         ACT SILE
                            1158
                                        1158
                                                           BY SIMILARITY.
                                                           PROSPHORYLATION (AUTO-) (BY SIMILARITY).
                                        1189
1177
         MOD_REG
                            1189
                                                           EVWCPARPTATAHOOVY LPCCRLPCRPYALMAKYI
         VARGILLIC
1 T
                             222
FΤ
                                                            (IN ISOFORM 3).
1.1
        VARGETIC
                                          . 3
                                                           VW. MARETATAHOUVY - RVVA JABBYI (IN
EТ
                                                           ISOFORM 2).
                                                           MICSING (IN ISOFORM 2 AND ISOFORM 3).
ETT
         VARGPLIC
                              284
                                          173
                                                           CETTOBER : CAPRVOPAC (IN ISCEORM 2 AND
         VARGOUST
L'T
                                          152
                             4 14
FT.
                                                           ISOFORM 3).
         VARSPLIC
                             54.34
                                         4.46.
                                                           MISSING (ÎN ISOPORM 2 AND ISOPORM 3).
FT
                                         673
                                                           ASASPIEACOSCLULLER - GLSQPHRSLRELLAACWNS
FT
         VARSPLIC
                             Fy 1, F,
                                                           (IN ISOFORM 2 AND ISOFORM 3).
UTTHLACEVIEMOCIAWREAEGLEGEREE
FT
                                        10.27
F'T
         VARIDURE
                            1000
                                                           PRDELCVACAGLYACQDPAIR (IN 180FORM 2 AND
E"T
FΤ
                                                           ISOFORM 3).
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VARSSILL
                        1299
                                   SETEGOPSAP - EPHDRPAFATESPOLDPLWRGRPG
                 12:00
                                    (IN ISOFORM 2 AND ISOFORM 3).
     MULAGEN
                                   A. OF LOSS OF ACTIVITY.
     POWER BO
                                   A \rightarrow A (IN REF. 2).
1 1
                  . .
                         6.0
                                   S \to P (IN REF. 3).
     NEMPORE.
                         128.
                                   G N (IN REF. 3)
     OF MELLIC
                         280
                  200
1-1
    CONFILIC
                  287
                         282
                                   MISSING (IN REF. 3)
     PENELTIC
                         4 903
                                   K - N (IN FEEL T).
    of While
                                   A - F (IN REF. 2 AND 3)
     " NELIC
                        50,00
                 37.4
                                   EL \rightarrow D\hat{V} (EN REF. 3)
                 1,000
                         1. 12
                                   A -- 1 (IN REF. 2 AND 1).
     ob Maride
     " NELIC
                 1,000
                         ficht t
                                   N \rightarrow Y (IN REF. +).
     PONELIC
                 1 ...
                         706
                                   I - N (IN REF. 3).
     A NELIC
                 7 - 4
                         7.44
                                   S - EW (IN REF. 2 AND 3).
     1 NELLEC
                 1
                                   R + S (IN REF. 1).
-Sd + QR (IN REF. 1)
     1 MEDIC
     ST JUENC
                 12 ← AA. 144 €14 MW: EFE2D6086AF3D100 (R064);
  griers Matics
                           -1.7%: Shore 9: DR I; Length 1299;
  Boot focas Schularity (100.5%) Fred. No. 0.97;
  Matthes ( ) inservative ( ); Mismatches ( ); Indeks ( ); Saps
      TO FIRVETADESCENDEN
          4. 1111
TO THE RVETADED 1179
FRS04.1 14
CHAMBE CHALLES
TO COMB ON TH
                    STANDARD;
                                    PRI;
                                             74 AA.
    ्कार उसके ह
    1 + 1 T
              1 \pmod{40}, Created)
    The certification (seef, 40), Last sequence appliate) or MAR 1702 (seef, 41), Last annotation update).
    Schooros me enzelope protein B (Chlorosome 7.5 kba protein) (Cderola:
     ⊃ison' -hiorosome protein).
- IN
     Chilorope as top idum.
     Northerna. Green scattur batteria: Thiordoram.
9800 Taxil Lock:
     DEQUENCY FROM N.A.
     Pland S., Frisk G., Züber H., Bryant D.A.;
     "Tenes empodiat two chlorosome components from the green sulfur
     parterna (Merobium vibriotorme strain 8837D and Chlorobium
     tequistur "
     Philosy: Res 41:261 275(1994)
D/N
    1.71
100
     · HARACI - FIZATI →N.
     METGINE 96421116; PubMed 8824146;
    Chang S. Rryant 10A.;
     "Thiracterial con of esmb genes, emcoding a 7.5 kbs protein of the
     chaoros we envelope, from the green sultur bacteria chlorobium
1. 1
     vibriof rmc 8327D and Chlorobium tepidum.";
     Arch. Microbiol. 186:234-244(1996).
      ! FUNCTION: COMPONENT OF THE PHOTOSYNTHETIC APPARATUS WHICH MAY BIND
         THE TELOR COME TO THE BACTERIOCHESIC WHYLE A PROTEIN MONOLAYER.
        SUBSELLOGAR I STATION, ENVELORE ENGLETH OF THE CHLOROSOME.
      * SIMPLARITY: BEGONGS TO THE COMBUSTOME FAMILY.
     1843 SWISS PROLECTLY is copyright. It is produced through a collaboration
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    sentables requires a license agreement (see http://www.leb.slb.b/add.case)
     or send as email to license (isb sub, ch).
    HARRY - Bolley AAB USeptil: AND INTE.
    Andost these a Bacterrochlorophyll; Repeat; Chicrosome.
    INCOME.
                         BY SIMILARITY.
                   7 6.0
    LOMA LN
                                  4 X APPROXIMATE REPEATS.
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16
     REPEAT
FT
     REPEAT
                  28
                          3.8
                                   2.
FC 1
     REPEAT
                  319
                         4.9
                  571
F1.1
     PEPEAT
                         6.13
                                   4
                        7477 MW; F5692F9143E167(@ CRC64;
     SHOUENCE
                74 AA;
                           1.5%; Score 8; DB 1; Length 74;
  Ouery Match
  Best Local Similarity 100.0%; Pred. No. 0.71;
  Matches 8: Conservative 0: Mismatches 0: Indels 0: Caps
       314 LOSVSSAI 321
         11111111
       63 LUSVSSAI 70
Diffi
RESULT 15
FIXX_RHIME
ID FIXX RHIME
                    STANDARD:
                                    PRT:
                                           48 AA
     P09822;
DT
     -01-MAR 1989 (Rel. 10, Created)
     -01-MAR-1989 (Rel. 10, Last sequence apdate)
     01-MAR 2002 (Rel. 41, Last annotation update)
     Ferredoxin-like protein.
GN
     FIXX OR RA0444 OR SMA0816.
     Rhizobium meliloti (Sinorhizobium meliloti).
     Plasmid pSymA (megaplasmid 1).
(H)
     Bacteria; Proteobacteria; aipha subdivision: Rhizobiaceae group;
     Rhizobiaceae: Simorhizobium.
\cap X
     NCBI_fax1D 382;
     [1]
     SEQUENCE FROM N.A.
     STRAIN 1021:
     MEDITINE 87137267; PubMed 3029021;
     Earl C.D., Ronson C.W., Ausubel F.M.:
      "Genetic and structural analysis of the Khizobium meliloti fixA,
     tixB, fixC, and fixX genes.";
     J. Bacteriol, 169:1127-1136(1987).
RT.
     [2]
     SHOUENCE FROM N.A.
WE
     MEDLINE 87165742; PubMed 3031010;
КX
     Dasha I., Kovalenke S., Banfilvi S., Kondorosi A.;
     "Rhizobium meliloti insertion element ISRm2 and its use for
     identification of the fixX gene.";
     J. Bacteriol. 169:1403-1409(1987).
RT.
кN
     1 4 1
     SEQUENCE FROM N.A.
RP
     STRAIN 1021;
КX
     MEDLINE 21396509; PubMed 11481432;
     Barnett M.J., Fisher R.F., Jones T., Komp C., Abola A.P.,
     Barloy-Hubler F., Bowser L., Capela D., Galibert F., Godzy J.,
     Gurjal M., Heng A., Heizar L., Hyman R.W., Kohn E., Kahn M.L.,
Kalman S., Keating D.H., Palm C., Book M.C., Sarzycki R., Wells D.H.,
     Yeh K. C., Davis R.W., Federspiel N.A., Long S.R.;
     "Nucleotide sequence and predicted functions of the entire
RT
     Sinorhizobium meliloti pSymA megaplasmid.";
     Proc. Natl. Acad. Sci. U.S.A. 98:9883-9888(2001)
      ! FUNCTION: COULD BE A BUE 48 CLUSTER CONTAINING PROTEIN.
      I SIMILARITY, TO FERREDOXINS PROM PSEUDOMONAS PUBLICA AND CLOSIBIDIUM
         TARTARIVORUM, PERREDOXIN I FROM ACETORACTER VINELANDII, PERREDOXIN
CC
         II FROM DESULFOVIBRIO DESULFURICANS.
CC
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     between the Swiss Institute of Bioinformatics and the EMBL outstation
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     use by non-profit institutions as long as its content is in no way
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     contitios regaines a license agreement (see http://www.lidecill.ch/ssc.acc)
(20
     or send an email to licensesisb sib.ch).
('('
DR
     EMBL: M15546; AAA21771.1;
DR
     EMBL; M15787; AAA26282.1;
     EMBL; AE007235; AAK65102.1; .
```

Job time: 329 sec

```
DR PIR; 126952; 126952.
DR PIR; A26933; A26943.

DR InterPro; 11R01450; 4Fe4s_ferredoxin.
DR PROSITE; PS00198; 4Fe4s_FERREDOXIN; 1.

DR PROSITE; PS00198; 4Fe4s_FERREDOXIN; 1.

KW Complete proteome.
FT CONFLICT 62 62 1 -> 1 (IN REF. 2).
FT CONFLICT 97 97 F -> S (IN REF. 2).
SQ SEQUENCE 98 AA: 10937 MW; 020101A9236402D8 CRC64;

Query Match 1.5%; Score 8; 18 1; Length 98; Best Local Similarity 100.0%; Pred. No. 0.93; Matches 8; Conservative 0; Mismatches 0, Indels 0, Gaps 0;

QV 528 RSPSLNLL 535 111.1(1)
Db 33 RSPSLNLL 40

Search completed: May 13, 2002, 21:35:29
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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Pun on: May 17, 2002, 21:22.16 , Scorch time 52.9% Seconds

(without alignments)

979 393 Million cell updates/sec

Title: US-09-445-223 1

Perfect score: 540

Sequence: 1 MNGEAICSALPTIPYHKLAD.....PEILVVSRSPSLNLiQNKSM 540

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 283138 seqs, 96089334 residuas

Word size . 0

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0

Maximum PB sei length: 2000000000

Post-processing: Listing first 45 summaries

Database : PIR_71:*

1: pirl:*

åi piråi∗

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMAPIES

Result.		Query				
No.	Score	Match	Length	DB	ID	Description
1	10	1 9	517	2	T23413	hypothetical prote
2	44	1 7	F 2	2	856723	SNF1 related prote
3	9	1.7	66	2	149118	ink 76 – mouse (fr
4	9	1.7	6.7	2	148695	gene nskl protein
5	14	1.7	416	2	T29805	hypothetical prote
6	49	1.7	417	2	133827	hypothetical prote
7	9	1.7	430	2	T33070	hypothetical prote
8	٠,	1.7	4 + 1	2	T29186	hypothetical prote
و٠	4	1.7	469	1	S17656	Ca2+/calmodurin-de
10	19	1.7	472	2	B90100	SNF-related kinase
1 1	1,4	1.7	473	1	S59941	serine/threonine-s
1.2	14	1.7	473	1	A53036	Ca2+/Calmodollin de
1 •	14	1.7	474	1	IVRTC4	Ca2+/calmodulin de
1.4	**	1.7	502	2	152637	Ca2+/calmodulin-de
15	ι,	1.7	504	2	T10449	probable scrinc/th
16	C.	1.7	511	1	A56009	serine/throomine-s
17	19	1.7	512	1	JC1446	sering/threoning s
18	*,	1.7	512	2	107788	probable scrine/th
19	* 1	1.7	562	2	T29858	hypothetical profe
2.0	14	1.7	5.76	2	r41587	probable carbon ca
23	1.	1.7	6 -2	2	272512	Pud2 protein yea
4 .	٠.	; -	6.47	1	Altenso	sering threening a
23	Ģ	1.7	용하극	2	F85343	hypothetical prote
2.4	14	1 7	971	2	140646	protein-tyru, line k
25	1,	1.7	881	1	148697	protein-tyrosine k
26	G	1.7	892	2	T08973	probable scrinc/th
27	9	1.7	946	1	A47299	ror related recept
28	9	1.7	1099	2	S4805+	protein tyrosine k
29	L _a	1 7	1100	2	843677	protein tyrosine k

30	9	1.7	1124	2	A55747	L-JAK protein-tyro
3.1	٠,	1.7	1299	2	158401	protein tyrosinė k
3.2	8	1.5	4 +	2	вз4711	kinase-related pro
3.3	8	7.5	4.9	2	041615	G protein-coupled
3.4	8	1.4	5,0	2	:38226	protein-tyrosine k
35	8	1.5	5.2	2	856722	SNF1-related prote
3.6	8	1.5	e, , ,	ż	\$66324	protein kinase AKl
3.7	8	7	53	1	FERMX	te:redoxin [4Fe-48
3.8	8	1.5	98	ż	1/95317	FixX terredoxin=1;
3.9	Ω	1.6	1771	- 2	851021	protoin kinggo PPK
4.0	8	1.5	101	2	S51162	protein kinase PRK
4.1	8	1.5	1.2	- 2	A45950	AMP-activated prof
4.2	8	1.5	14.4,	2	112201	probable ede⊋ like
4.3	8	1.5	174	2	001743	AMP-activated prot
4.4	н	1 . r.	281	2	PC4220	protein kinase (E°
4.5	8	1.5	291	2	145698	hypothetical prote

ALIGNMENTS

```
RESULT 1
123413
hypothetical protein K07F5.4 Caemorhabditis elegans
C;Species: Caenorhabditis elegans
C;Accession: 12341⊀
R:Hembry, €.
submitted to the EMBL Data Library, March 1996.
A:Reference number: Z19738
A;Accession: 123413
Aprilative great Consequence Cate Control ON, TMPC, CODBJ.
A; Molecule type: DNA
A; Residues: 1.517 - WILL
A;Cross:reterences: EMBL:27c284: PICN:CAA94277.1; CDPDB:DN00922; CESP:K07F5.4
A, Experimental source. close K07F5
C:Genetics:
A:Gene: CESP:K07F5.4
A: Map position: 4
A: Introne: 41, 2 (22), 6 (26), 78, 324, 2 (444, 3)
C) Superfamily: protein tyropine kinase see: protein kinase homology: SW2 homology: SW
  Query Match 1.9%; Score 10; DB 2; Length 517; Bost Local Similarity 100.0%; Pred No. 0.16;
  Matches 10: Conservative 0: Mismatches
                                                   0. Indels 0. Gaps 0:
      160 VKIADECLSK 169
          296 VKIADPGLOK 195
RESULT 2
$56723
SNF1-related protein kinase (EC 2.7.1. ) (clone Aspk3) - pat (fragment)
C. Species. Avena sativa (eat)
C, bate. 27 Set 1995 #sequence_revision 19 Jan 1996 #fext_change 18 Sep 1997
C:Accession: 056723
R.Huttly, A.K.; Phillips, A.L.
Plant Mol. Biol. 27, 1043 1052, 1995
A.Title, differellin regulated expression in out alcorone cells of two kinases that s
A; Reference number: $56638; MUID: 95284341
A; Accession: 356723
A; Molecule type: mkNA
A, Moniduer: 1 12 < HUI:
 through the distribution of the partition of the property of the kineses, problem kinese home
C; Keywords: phosphotransferase; protein kinase
F, 1 f2,70 mail: plotein kinase hold int, (fragment) Fig:
  Query Match 1.7%; Score 9; DB 2; Tenath 52; Best Local Similarity 100.0%; Pred. No. 0.18;
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Matches 9; Conservative 6; Mismatches C; Indels 0; Gaps

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THE VK ALEBBA 168
          - f - T - T
       The VK. ADDOLL TR
4-120HLT - 3
119118
ink 76 - mou o (fragment).
* Spections Missimus alus (nouse mouse);
Collistics and A.A. 1999. #Seephenice revisions on that I note #text_ Sample _1 top. Text.
C:Accession: 149119
e. Siyaneva, a Y.: certiso M.S., Marel I.A.: Tyner, A.L.
incorporate T_{ij} , S_i \leftarrow 2^{-i} T_i [1904]
Allither Tyr time kiname gene expression in the mouse small intestine.
A. Reference comber 149118; MUID: 94268846.
A. Actions from 1.14 +11e.
Addition processinary; translated from GB/EMBL/DDBJ.
A: Molecule tipe: mENA
A:Residues: 65 - FES+
Applies references EMBL:U13258; NIL:q532727; PIDN:AAB60447.1; PID:q532728
3) Superfamil: unassigned SerZthr or Tyr specific protein kinases; protein kinase homold
Fit 56/Domain: protein kinase homology (fragment) KIN
  Query Match
                           1.7%; Score 9; DB 2; Length 66;
  Query Match 1.7%; Score 9; DB 2;
Rept Local Similarity 100.0%; Prod. No. 0.23;
  Must be a continue analysis of the Million beautiful indicts of the days of
    150 VK.ADFGL. 168
        H. VK. AGFORD 23
61.300 . 4
 126600
dene noki pr bein - mouse (fragment).
 'a Specialisa: Mademus ralud (house modse);
 Tribate i coloritati 1990. #no que ne e la evizar an Succial 1996. #terkt je haroge (24. Bep. 1999).
Pakeatha All
Manner Senione (*), *** (*) Loste
Addition (Securitor and chromosomal location of NBEL), positional operation religion
Asketerence sumber 148005, MCIL,56061305
ArAcher sion (14869)
AuStalian preliminary: translated from GB/EMBL/DDBJ.
As Modernate to pace menA.
A: Periodues: 1 57 RES-
Astrons refreement EMPL:X:00.007, NIC 41 01006, 140N.CAA60127.1, 140,41001886
 in lenethers:
Addeno Nskii
 Supertamic. The staned Set/Thr or tyr specific protein kinases; protein kinase homodo
 1 6 Doma. protein kinase bomology (fragment) (KIN)
                           Tilter Schire Gro DB vir Dength 67;
  pager. Mat
  Best Local Administraty | 170, (A) Prod. No. 0.23;
  Matches () Conservative 0; Mismatches 0; Indels 0; Gaps 0;
IN THE VE ALREID LINE
       TO VERADEGLO 25
FESULT 5
1,09800
apportant real projects on (125Ax.5). Then a habit its elegans.
happened a contribution of equals :
Subate 15 of 1900 #sequence revision 15 oct 1999 #text change 31 Jan 2000
NACTOR OF THERE
enhatrealte or poteliyes. L.
Submitted to the EMBL Data Library, June 1996.
Asbestriptics, the dequence of the degans cosmid 125A8.
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A:Reference number: Z20689
A; Accession: T29805
Auttatus, proliminary, translated from SP/EMPL/DDR-C
A: Molecule type: DNA
A: Residues: 1 416 · LAT ·
A:Cross references: EMBL:061950: FIDN:AABUCISCLI: SPERISINSUU22: CESPICZ5AB.5
A; Experimental source, strain Bristol N2, clone C. A8
C:Genetics:
A;Gene: CESP:C25A8.5
A; Map position: 4
  all afternacy in the company of the party of
C; Superfamily: protein-tyrosine kinase sic; protein kinase homology; SH2 homology; SB
      Query Match
                                                                               1.7%; Score 9; DB 2; Length 416;
      Best Local Similarity 100.0%; Fred. No. 1.4;
      Matches 9; Conservative 0; Mismatches 0; indefs 0; Gaps \phi
                  160 VKIADEGLS 168
                         111111111
                  258 VKIADEGLS 266
RESULT 6
T33827
hypothetical protein F23C8.7 - Caenorhabditis elegans
C:Species: Caemorhabditis elegans
  t, Hate: 19 % t 1999 #se pence_re.lslsn. 29 % t 1999 #text change 31 Jan 2000
C; Accession: T33827
R:Miller, N.: Wamsley, P.
submitted to the EMBL Data Library, November 1998.
A; bescription: The sequence of C, elegans cosmid \pm 2.808.
A; Reference number: 221419
A; Accession: F33827
A: Status: proliminary; translated from CR/EMBL/DDRG
A; Molecule type: DNA
A; Residues: 1-417 < MIL >
A; Cross references: EMBL: AF106583: FIDN: AAD03135.1; GSF44::GN00019; CESP: FLOCE.
A.Experimental source, strain Bristol Nz. clone P. 308.
C:Genetics:
A; Gene: CESP; F23C8.7
A: Map position: 1
A_{n}(t)n^{\frac{1}{2}}(t^{\frac{1}{2}}n) = \frac{1}{2}(2^{n}t^{\frac{1}{2}} + 6n^{\frac{1}{2}}t^{\frac{1}{2}} + 1)(n^{\frac{1}{2}}t^{\frac{1}{2}} + 1)(n^{\frac{1}{2}}t^{\frac{1}{2
Comportantly, protein tyropine kluane dr., grotein kluane boology. TH2 homology: SH
                                                                               1.7%, Score 9, DB 2, Length 417;
      Query Match
     Best Local Similarity 100.0%; Pred. No. 1.4;
      Matches 9, Conservative 0, Mismatches 0; Indels 0: Japs
              160 VKTADEGLS 168
                             RHHH
Lib
                 258 VKTADEGLS 266
RESHLE 7
hypothetical protein C35E7.10a - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 29-oct-1999 #sequence_revision 29 oct 1900 #text;change 04 Mar 2000
C;Accession: T33070
R;Graves, T.; McDonald, R.
submitted to the EMBL Data Library, May 1998.
A;Description: The sequence of C. elegans cosmid 1987.
A; Reference number: 221278
A; Accession: T33070
A:Status: preliminary; translated from dB/EMBL/DLECT
A; Molecule type: DNA
A; Residues: 1-430 - GRA -
Ajdross references: EMBL:AF067216; PHDN:AAC17525...; GSFDB:GN00019; CESP:COF7.1.4
A; Experimental source: strain Briston NZ; clone C GE7
C;Genetics:
A; Gene: CESP:C35E7:10a
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A:Map position: 1
A total: 1 1204 TTD: 18108, 2800 98503 985
Cosupertamily: protein typesine kinase sre, protein kinase bomedagy, SH2 bomedagy, SH3
  Query Match 1.79, Source 9, DR 2, Compth 430, Best Local Similarity 100.09; Pred. No. 1.4; Matches 9, Conservative 0, Mismatches 0, 1.4:8
                                                      0 154-15
                                                                     0, 045 0.
      160 VETADECTS 168
      261 VEIALFOLS 269
RESULI 8
129186
hypothetical pratein C55C3.4 - Caenorhabditis elegans
C; Species: Caencihabditis elegans
C;Date: 15-0ct-1990 #sequence_revision 15 (+ : 1990 #text_chang- 04 Mar 2000
C:Accession: 129186
R; Woessne, J.; Stellyes, L.
submitted to the EMBL Data Library, April 1996.
A:Description: The sequence of C. elegans cosmid C55C3.
A; Reference number: 220585
A; Accession: 129186
A: Status: preliminary: translated from CBATRO ADPT
A; Molecule type: DNA
A; Residues: 1-431 < WOE>
A:Cross-references: EMPI-UE-235: PIDN:AAA09 63.1, OSPDB.GNC0022, GEFF.G5502.4
A:Experimental cource: strain Bristol ND; c one C55C3
C:Cenetics
A:Gene: CESP:C55C3.4
A:Map position: 4 A Introdes 22 PP = 77 PR = 192 PR = 146 [x = +65, x = +3]/3
C; Superfamily: protein-fyrosine klease are protein kinase homology; SH2 homology; SH3 !
  Query Match 1.7%; Score 9; DB 2; Length 431; Best Local Similarity 100.0%; Prod No 1 4;
  Matches 9: Conservative 0: Mismatches
                                                      0; Indels 0; Caps
      160 VKIADFGLS 168
          111111:111
      261 VKIADFGLS 269
RESULT 9
Ca2+/calmodilin-dependent protein kinase (8: 2.7.1.123) (V mouse
C; Species: Mus musculus (bouse mouse)
C:Date: 10-Sep-1999 #sequence_revision 10-S-p-1999 #text change 10-Sep-1999
C:Accession: S17656; A29878; 149571
R; Jones, D.A.: Glod, J.; Wilson-Shaw, D.; Hahn, W.E.; Sikela, J.M.
FEBS Lett. 289, 105-109, 1991
A:Title: CDNA sogness and differential expression of the mouse Ca(2)/Calmodulin-depend
A; Reference number: S17656; MUID: 91372388
A: Accession: S17656
A; Molecule type: mRNA
A; Residues. 1 165 UCN>
A:Cross references, FMBL,X58995, NID.450366, FIDN.CAA41741.1, FID.450367
R;Sikela, J.M.; Hahn, W.E.
Proc. Natl. Acad. Sci. U.S.A. 84, 3038-3042, 1987
A: Little: Screening an expression library with a ligand probe: isolation and segumee of
A:Reference number: A29878; MUID:87204263
A; Accession: A29978
A; Molecule type: mRNA
A; Residues: 315 469 < SIK =
A; Cross-reterences: GB: M16206; NID: q200360; PIDN: AAA39933.1; PID: q387512
R:Sikela, J.M.; Law, M.L.; Kao, F.
Genomics 4, 21-27, 1989
A) Fittle: Chromosomal localization of the homan gene for brain du2//sulmodulin-depend nt
A; Reference number: 149571; MUID: 89122027
A: Accession: 149571
```

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A; Status: proliminary, translated from CB/DMBL/DDBJ
A.R. No. 15. (pp. maPMA)
A.R. M.L. 250 277, (pp. 172) 271, (pp. 172), (pp. 172) 172, 173 174, (46) 4898
A.Cross references: 38:173857; NID. 4192366, PIDN. AAA37 66.1; PID: 4192367
A; Experimental source: brain
C. Superfamily. Call, Calmodulin dependent protein kinase, protein kinase homology
C: Keywords: alternative oplicing; ATP, calmodulin binding; phosphotransferase; serine
P.40 206, Tempain, protein kinage har 1, year EIN>.
F;48-56/Region: protein kinase ATP binding motif
P: 306 - 469, Oroduct: calepormin #statur predicted (CSP)
F:318 337/keylon. ca.modulin binding #status predicted
F;71/Λctive dite: Lys #status predicted
  Query Match
                             1.7%; Score 9; DE 1; Length 469;
  Best Local Similarity 150,0%; Fred, No. 1.5;
  Matches 9, Conservative 0, Mismatches 3, Indels 0; Gaps
      161 KIALFGISK 169
          1111111
Db
      178 KIADFGLSK 186
RESILL LO
B90100
CME-rolated kiname (imported) - Caillardia that a run-nemorph
C; Species: nucleomorph duillardia theta
A: Note: a nucleomorph in the vestigial nucleus of a ensuryotic endosymbiont
5, hate. 10 May 2001 was pierre greeislan 10 May 2001 wheat_bhands 15 dlm 2001
C;Accession: B90100
RyDonglas, S.; Zaumer, C., Fraunholf, M., Beaton, M.; Penny, S.; Deng, L.F.; Wu, X.;
Nature 410, 1091-1096, 2001
A; Title: The highly reduced genome of an enslaved alga, nucleus.
                     Appropriate recover content
A; Accession: B90100
A; Status: preliminary
A: Molecule type, DNA
A; Residues: 1-472 DOUS
A, Cross reterences, CB, AF165818, NID.g13794554; FIEN: AAK39929.1; GSPDB: GN09150
C:Genetics:
A:Gene: kin(snfl)
A: Map position: 1
A; Genome: nucleomorph
C: Superfamily: AMP-activated protein kinase; protein kinase homology
C; Keywords: nucleomorph
  Query Match 1.7%: Score 9: D8 2: Length 472: Best Local Similarity 100.0%, Fred. No. 1.5: Matches 9: Conservative 0: Mismatches 0: Indels 0: Gaps
    160 VKIADEGLS 168
           STREET
    149 VKIADEGLS 157
RESULT 11
$59941
serime/threonine specific protein kinase (EC 2.7.1. ) EKIN2 - barley (fragment)
C. Species. Hordern valuate (barley).
C;Date: 15:Feb:1996 #sequence_revision 01 Mar 1996 #text_change 26:Feb:1999
C; Accession: S59941
R;Hammappel, U.: Vicente-Carbajesa, L: Birker, U.B.A.; Shewry, P.K.: Halford, N.J. Plant Mol. Blot. 27, 1235-1240, 1995
A, Title, Bifferential expression of two barley SNP1 related protein kinase genes.
A; Reference number: $59.41; MUID: 95284374
A; Accession: S59941
A; Status: preliminary
A, Molecule type, mKNA
A; Residues: 1:473 - EAN
A, Cross references: DMRD. X82548
A; Gene: BKIN2
```

```
A:Description: Citalyses the formation of peptidyl serine phosphate or peptidyl threoniq
Compertantly: AMP activated protein kinase; protein kinase homology.
otrKeywords. Alto magnesiumo phosphotransteraség serine,⊄threesine spécitic proteis ∗inas∢
Fig. 1 (1944, 50) and the property of the state of the first property of the first
Fig.1.40.11 .117/Active site: Lys, Slu, Asp. Lys #status predicted
F:12 < 124/ (indin) site: magnesium (Asn. Asp) #status predicted
                            1.7%; Score 9; DB 1; Length 473;
  Querry Materia
  West Local Sub Larity (100,0%) Prod. No. 1.5;
  Matches of the Connection of
                                   to Maramat Lege of Endelse G. Sapar C.
      150 VKTADESTS 168
         100,140,03
       129 (BIALF U.S. 15)
RE2001 1 1.
AS COLD
Carry calmost trip dependent protein kinase (EC 2.7.1.124) [V human
N:Alternate name:: Call/Calmodulin dependent protein kinase Gr; CaM kinase IV
C:Species: Home Laplens (man)
 CiDate: It Sep 1 cd #sequence revision to Sep-1999 #text change 16:Jun-2000
C:Accession: A53 th: JC2261: 153768
R:Modicatos G.: Hamissian, S.H.: Jawahar, S.: Vara, L.: Kieff, E.: Chatifa, T.A.
1. Vinol. (* 16+1-1705) 1994.
A:lit.e: A ligz:,/calmodulin-dependent protein kinase, fam kinase Gr. expressed after tr
A; Reference number: A53036; MUID: 94149862.
At America Leading As a loss
Applications of realiminary
A:Mosemale type: 00RNA
A:Remidues 1.47 - MSGs
A.Creuss references: GB:L24959; NIE:q407006; PIDN:AAA18251.1; PID:q407006
ByKitania, a reskutos Bay Pajasawa, H
J. Roschem (115, +37,640, 1994)
A; Little: c. NA clening and expression of human calmodulin dependent protein kinase LV.
A; Reference number: 02204; MUID:94-036404;
At A Scenarios ( 1812. 61)
A; Movemble type: %RNA
A; Repudues | 1 470 × Kii +
Apthologic references: SBs1830742; NIL::4487998; PIDN:BAA06403.1; PID::4871845
Robbland, M. Mic McGroe, R.S., Chunstede, d.
demo (42), 131 191, 1994.
Arithle: The CDNA sequence and characterization of the Califordisabilin dependent protein
As Reference numbers (53768) M010:94252566
A:Acression (550)8
Addition, prolimning, translated from MC/TMRC/TDRC
A:Molecule type: mRNA
Arkenidnes 1 47: - RIB -
A:Cross references: GB:L17000; NID:q 006478; E:DN:AAA35639.1; Pff::q306479
ercomment: This protein is a Carr responsive multifunctional protein kinase, which occur
s system and in the immune system.
Applement GDE 11.K.
A;Cross reterences: GDB:6155815; OMIM:602366
A:Map position: Hpl5.5 Hpl5.4
TrSuperitum: yr Carly/Sulmodillin dependent protein Kinane, protein Kinane homology
 TKerkerds Aft: Aftraw binding: culmodulin binding; phosphoprotein; phosphotransterasd
F:44 COZDC sain: protein kinase homology - KIN -
F:5. PayRess and protein kinase ATP binding motif
1:3.5 323/Estron: Salwodelin binding #status predicted
F:864. 15/Essiling safes phosphate (Ser) (ovalent) #status predicted

    I. Org. Physics Fr. DB Ir. Length 473;

  Best Local Sami grity (100,0%) fred, No. 1.5;
  Matches 9: Conservative 0: Mismatches 9: Indels
       COLOR ATTOMAKATOR
              . 1.7
      THUS K ALDRESS K 1900
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RESULT 13
TVRTC4
Sazi, Grahme duling dependent prefete kinase (EC 2.1.1.123) IV i rat
M. Alternate rame for a planed alle dependent protein & hase Gr
N, Contains: calspermin-
C; Species: Rattus norvegicus (Norway rat)
C:Date: 31-Mar 1993 #sequence_revision 31 Mar 1993 #text change 11 Jun 1994
C; Accession: A41103; A41237; A32865; A41250; A3.035; A60255; 153706
R;Ohmstede, C.A.; Bland, M.M.; Merrill, B.M.; Sahyoun, N.
Proc. Natl. Acad. Sci. U.S.A. 88, 5784-5788, 1991
A.Title: Relationship of genes encoding Ma(2))/ almodilin dependent ji term kimuse Mo
A; Reference number: A41103; MUID: 91288548
A; Accession: A4110+
A:Molecule type: DNA
A; Residues: 47 141, 'NE', 144 474 + OHL+
A;Cross references: GB:M74488; NID:q203219; PIDN:AAA40845.1; PID:q203220
A; Note: this sequence has been revised in reference A41237
A: Note: part of this sequence was confirmed by sequencing of cDNA to mRNA
R; Ohmstede, C.A.; Bland, M.M.; Merrill, B.M.; Sahyoun, N.
Proc. Natl. Acad. Sci. U.S.A. 88, 9375, 1991
A; Reference number: A41237
A; Accession: A41237
A; Molecule type: DNA
A: Residues: 142 143 + 0H2 +
A; Cross references: GB:M63334
A: Note: this is a revision to the sequence from reference A41103
R;Ohmstede, C.A.; Jensen, K.F.; Sahyoun, N.E.
J. Biol. Chem. 264, 5866 5875, 1989
A; Title: Ca(2))/calmodulin dependent protein kinase enriched in cerebellar arabble se-
A; Reference number: A+2865: MUID:89174647
A; Accession: A32865
A; Molecule type: mRNA
A; Residues: 250 474 - OH3 -
A;Cross references; GB:304600; NHD:q206172; PHD:AAA41867.1; PHD:q204173
R; Means, A.R.; Cruzalequi, F.; LeMaqueresse, B.; Needleman, D.S.; Slaudhter, J.E.; 5
Mol. Cell. Biol. 11, 3960-3971, 1991
A; little: A novel Ca(2)/calmodulin dependent protein kinase and a maje germ real spec-
A; Reference number: A41250; MUID:91304387
A; Accession: A41250
A; Molecule type: mRNA
A; Residues: 1:371,'M', 373-408,'Q',410:474 - MEA -
A: Cross references: GB:M64757
R;Ono, I.; Slaughter, G.R.; Cook, R.G.; Means, A.R.
J. Biol. Chem. 264, 2081-2087, 1989
Affitle: Molecular cloning sequence and distribution of rat calspermin, a high affiliation
A; Reference number: A32035; MUID:89123272
A, A ++ 35 ion : A32035
A: Molecule type: mRNA
A:Residues: 306 371, 'M', 373 474 + ON1>
A:Cross references: GB:J04446; NID:q203642; PIDN:AAA40990.1; PID:q203643
R, uno, T., Means, A.R.
Adv. Exp. Med. Biol. 255, 263-268, 1989
A;Title: Calspermin is a testis specific calmodulin binding protein closely to dead to
A; Reference number: A60255; MUID: 90144189
A; Accession: A60255
A: Molecule type: protein
A; kepidues: 335 363 -- m2
A: Note: the amino end of calspermin was blocked
R:Bland, M.M.
Gene 137, 351:352, 1993
A:Title: Identification of alternate 5' untranslated regions in the gene encoding Ca.
A; Reference number: 153706; MUID: 94131312
A:Accession: 153706
A, Status, preliminary, translated from CB/EMBL/DOBJ
A: Molecule type: DNA
A:Residues: 1-37 - RES
A;Cross references: GB:L16999; NID:q310086; PIDN:AAA17443.1; PID:q310087
cycomment: Ca2/Caleedalie dependent protein kinese IV is enriched in cerebeilar arm.
and in sperm cells.
C:Supertamily: Ca2:/ealmodulin/dependent protein kinupe; protein kinuse homology
C:Keywords: alternative splicing: ATP: calmodulin binding: phosphotransterase: series
```

F:40 296/Domain: protein kinase homology · KIN·

Qy 160 VKIADFGLS 168

```
F:48-57/Region: protein kinase ATP-binding motif
F; '96 474/Froduct, calspormin #status predicted CSP.
F: 118-337/Region: calmodalin binding #status predicted
F:71/Active site: Lys #status predicted
  Query Match 1.7%; Score 9; 08 1; Length 474; Best Local Similarity 100.0%; Pred. No. 1.5;
  Matches 9; Conservative 0; Mismatches 0; Indexs 0; Gaps
      161 KIADEGLSK 169
           THEFT
      178 KIADEGLSK 186
RESULT 14
152637
\texttt{Ca2+/calmodilin} \  \, \texttt{dependent} \  \, \texttt{protein} \  \, \texttt{kinuse} \  \, \texttt{IV} \  \, \texttt{octa} \  \, \texttt{polypeptide} \  \, \texttt{-} \  \, \texttt{rat}
C; Species: Rattus sp. (rat)
C:Date: 26-Jul-1996 #sequence revision 26 Jul 1996 #text change 18-Jun-1999
C; Accession: 152637
R;Sakagami, H.; Kondo, H.
Brain Res. Mol. Brain Res. 19, 215-218, 1993
A:Title: Cloning and sequencing of a gene enroding the beta polypeptide of Ca2-/calmocul
A:Reterence number: 152637; MUID:94018484
A; Accession: I52637
A; Status: preliminary; translated from GB/EM3L/DDBJ
A; Molecule type: mRNA
A; Residies: 1-502 <RES>
A:Cross-references: GB:S65840: NID:q425383; HDN:AAB29372.1; PID:q425384
C; Supertami.y: Ca2+/calmodulin-dependent pro ein kinase; protein kinase homelogy
C; Keywords: ATP; calmodulin binding
F:68-324/Demain: protein kinase homology <KTD
F;76-84/Region: protein kinase AIP-binding notif
                            1.7%; Score 9; FB 2; Length 502;
  Query Match
  Best Local Similarity 100.0%; Pred. No. 1.6;
  Matches 9: Conservative 0: Mismatches 0: Indels
                                                                    0: Gans
      161 K:ADFGLSK 169
           111111111
      206 KIADFGLSK 214
T10449
probable serine/threenine-specific protein k mase (EC 2.7.1.-) - cucumber
N; Alternate names: SNF1-related protein kinase
C; Species: Cucumis sativus (cucumber)
C:Date: 16-5.1-1999 #sequence_revision 16-Jr -1999 #text_change 20 Jun-2000
C:Accession: T16449
R;Gumpel, N.J.
submitted to the EMBL Data Library, December 1996
A:Reference number: 217020
A:Accession: T10449
A; Status: preliminary; translated from GB/EMIL/DDBJ
A: Molecule type: mRNA
A: Residues: 1-504 < GUM>
A; Cross-references: EMBL:Y10036
A; Experimental source: cv. Masterpiece; cotyledon
C: Function:
A:Description: data yzes the formation of pertidyl-serine phosphate or poptidyl-thronum
C:Keywords: ATP: phosphotransterase; sering/threoning-specific protein kinase.
F:6-260, thomain frotein kinase horology (KIN>
                            1.7%; Score 9, 18-2, Length 504;
  Query Match
  Best Local Similarity 100.0%; Pred. No. 1.6;
  Matches 9; Conservative 0; Mismatches 0; Indels 0; daps
```

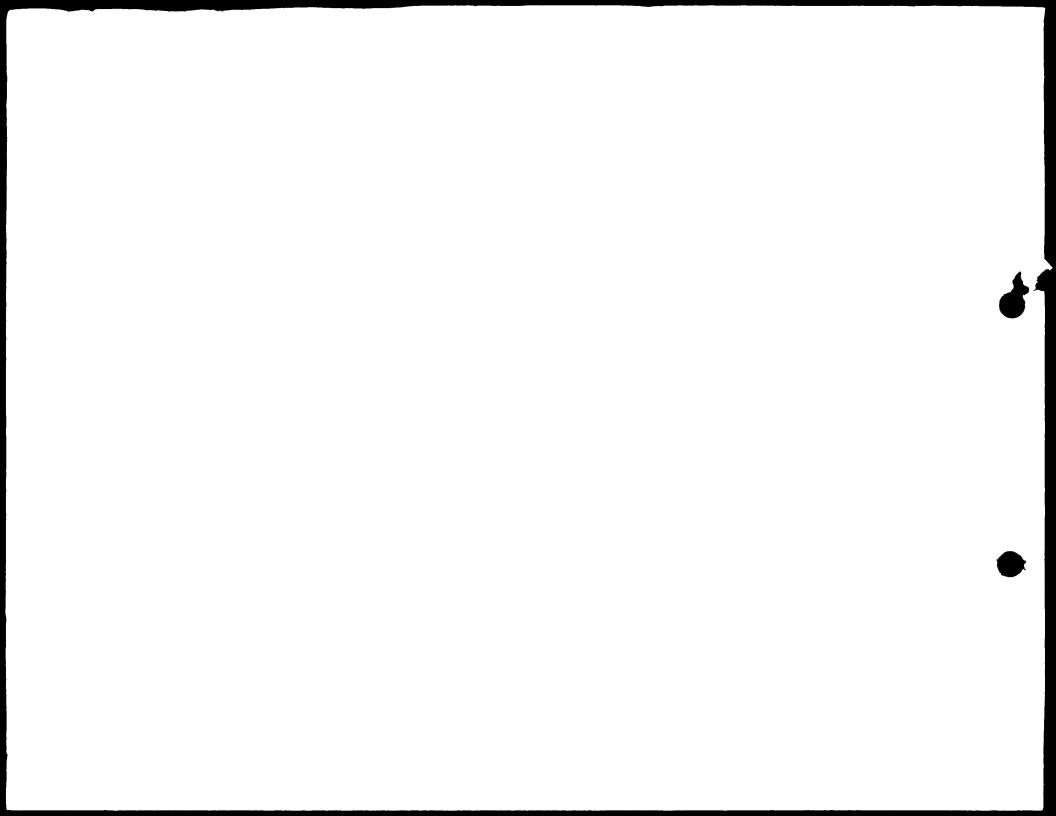
Search completed: May 13, 2002, 21:34:44 Job time: 658 sec

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160 VKIALFGLS 168
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 RESULT 5
 149118
 ink 76 - mouse (fragment)
 C:Species: Mas masculus (house mouse)
 C:Date: 02-Jul-1996 #sequence_revision 02-Jul 1-96 #text .danar 24 day 1999
 C:Accession: 149118
R;Siyanova, E.Y.; Serfas, M.S., Mazo, I.A.; Tyter, A.L. Oncogene 9, 2053-2057, 1994
 A: Title: Tyrosine kinase gene expression in the mouse small intestine.
 A; Reference number: I49118; MUID: 94268846
 A:Accession: 149118
 A; Status: preliminary; translated from GB/EMBL/ILBJ
A; Molecule type: mRNA
A; Residues: 1-66 <RES>
 A:Cross-references: FMRI :U13258; NID:3532727, P.DN.AABC0447.1, FID:4532728
 C:Superfamily: unassigned Ser/Thr or Tyr-specif c protein kinases: protein kinase home.
 F:1-66/Pownin: protein kinase homology (fragment) CKINS
  Usery Match. 1.7%: Score 9: DB 1: Dength 66: Best Local Similarity 100.0%: Pred. No. 0 13:
  Matches 9; Conservative 0; Mismatches 0; Indels
                                                                  U; Gars
       160 VKIADEGLS 168
           1111 111
        18 VKIADFGLS 26
 RESULT 4
 148695
 gene nskl protein - mouse (fragment)
 C; Species: Mus musculus (house mouse)
 C:Date: 02-Jul-1996 #sequence_revision 02-Jul 1:96 #text_change 24-Sep-1999
C; Accession: I48695
 R:Reith, A.D.
 Mamm. Genome 6, 689, 1995
 A; Title: Isolation and chromosomal location of Askl. a novel murine putative receptor ty
 A; Reference number: I48695; MUID: 96081359
 A; Accession: I48695
A; Status: preliminary; translated from GB/EMBL/DDBJ
A: Molecule type: mRNA
A; kesidues: 1-67 <RES>
A:Cross references: EMBL:X86367, NID:g1e31865; HEN:JAA63127.1: Fib:g1e 1886
C:Genetics:
A:Gene: Nskl
C; Supertamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase monob
F:1-67/Domain: protein kinase homology (tragment) :KIN.
  Query Match
                            1.7%; Score 9; DB 2; Length 67;
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            9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
      160 VKIADEGLS 168
       17 VKIADFGLS 25
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T29805
hypothetica: protein C25A8.5 - Caenorhabditis elegans
C)Species: Caenorhabditis elegans
C:Date: 15-Oct:1999 #sequence_revision 15-Oct:1999 #text_change (1-Jan 2000
C:Accession: T29805
R:Latreille, P.; Stellyes, L.
 Submitted to the EMBL Data Library, June 1996
    Peription: The sequence of C. elegans cosmid 025A8.
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A; Reference number: Z20689
 A:Accession: T29805
 A; Status: preliminary; translated from DE/EMEL/Class
 A: Molecule type: DNA
 A; Residues: 1 416 <LAL>
 A):Restance: 1 410 STATE
A):Cross-reterences: EMBLEME 1956- EIDN:AABC+15+... (Splice No. 120 MESPEC25AR.)
A:Experimental source: Strain milstel No. clone (15A8
  l:Genetics:
 A; Gene: CESP:C25A8.5
 A:Map position: 4 A:Titions: 22/4, 62/4, 129/4, 66/1, 814/4.
 hosupel rami Tyć proteri-hyd kille kilikao zi mija mila kille na li aji mila kille kille na li aji mila kille k
   Query Match
   Outery Match 1.76: Score in the Li Lemin 4.0: Best Local Similarity (00.0%) Fred No. 1.45 Matches 9: Conservative (00.000 Micrateles 00.000)
       THE VELADERIES IF 9
             Tradition I
 145 258 VKTADEGLS 266
 RESULT 6
 133827
 hypothetical protein F23C8.7 - Jackbrhardlis elemins
C:Species: Caemorhabditis elegans
C:Sate: 29:001-1999 #sequence_remarks Limits live #tixt_change virJan-2006
 C:Accession: T33827
R:Miller, N.: Wamsley, P
 submitted to the EMBL Data Library. November later
 A; bescription: The sequence of C. elegans assure in the
 A: Reference number: 2214.9
A; Accession: 133827
 A:Status: preliminary: translated trop im/EMBL/CIBC
A; Molecule type: DNA
A:Residues: 1-417 <MIL.
A; Cross-references: EMBL. AFTO/583. BITN-AAL SIMPLIF THIS IN THE HEAT B. + two
A) Experimental source: strain Bristo, Not obline Facts
C; Genetics:
A:Gene: CESP:F23C8.7
A; Map position: 1
A:Introns: 22/3; 60/3; 138/3; 43/2; 43/4;
 CrSupertumily: protein-tyresine kinase arm protein kinase om lag. Online ...
  Query Match. There were consequenced as Best Local Similarity (100.0%) Prod. No. 1.4:
   Matches to Conservative

    Mishat mas

     DIE VELADENIS 158
            1:121111
       258 VKIADESLS 16:
RESULT 7
hypothetical protein C3°E7.10; - Temporhabditis oforas
d Species: Caenornabuitis elegans
C Date: 29-Oct-1999 *sequence_revision 2-cost-1000 *rest of mine of Mar-2000
- Accession : 133070
R; Graves, T.; McDonald, R.
submitted to the EMBL Data Library, May 1998
A:Description: The sequence of C. elegans cosmid '95E'. A:Reference number: Z21178
A:Accession: 133070
A. Status: pre.iminary: translated in a. Ma/hMh./iie:
A:Molecule type: DNA
A:Residues: 1:430 < GRA-
A:Cross-references: EMBL:AF)67/10: PIDN:AAC17525.1: GSPLB.3N.J.:19: PESPLE-SET.15a
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A:Gene: CESP:C35E7.loa
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CURRENT FILING DATE: 1998-06-17

PRIOR FILING DATE: 1998-02-06

PRIOR APPLICATION NUMBER: 09/019,942

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             80 PILGICNEPEFLGIVTEYMPNGSLNELLHRKTEYPDV/WPLRFRILHEIALGVNYLHNMT 139
                 70 PILGICNEPEFLGIVTEYMPNGSINEIIHPKTEYPDV/WPLPFRILHEIALGVNYLHNMT 129
 Ðb
           140 PPLLHHDLKTQNILLDNEFHVKTADFGLSKWRMMSLSOSRSSKSAPEGGTIIYMPPENYE 199
Οy
          Db
           200 PGQKSRASIKHDIYSYAVITWEVLSRKQPFEDVTNPLOIMYSVSQGHRPVINEESLPYDI 259
                 Db
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           260 PHRARMISLIESGWA 274
                 11101-10111111
Dh
           250 PHRARMISLIESCWA 264
 RESULT 10
 US-09-069-023-6
 ; Sequence 6, Application US/09069023A
; Patent No. 6348573
 : GENERAL INFORMATION:
     APPLICANT: Nunez, Gabriel
     APPLICANT: Inohara, Naohiro
     APPLICANT: Koseki, Takevoshi
     TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR IDENTIFYING APOPTOSIS
     TITLE OF INVENTION: SIGNALING PATHWAY INHIBITORS AND ACTIVATORS
     FILE REFERENCE: UM-03333
     CURRENT APPLICATION NUMBER: US/U9/059,023A
     CURRENT FILING DATE: 1998-04-27
     NUMBER OF SEQ ID NOS: 38
     SOFTWARE: Patentin Ver. 2.0
    SEO ID NO 6
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       TYPE: PRT
      ORGANISM: Homo sapiens
 US-09-069-023-6
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Db
              1 SRKAQDCYFMKLHHCPGNHSWDSTISGSQRAAFCDHKTTPCSSAIINPLSTAGNSERLQP 60
           434 GIAGOWIQSKRFDIVNOMTEACLNQSEDALLSRDLINKEDYELVSTKPTRTSKVRQLLDT 493
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           494 TDICGEEFAKVIVQKLKDNKQMGLQPYPEILVVSRSISLNLLONKSM 540
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US-09-099-041A-5
 : Sequence 5, Application Us/09099041A
   Patent No. 5340576
   GENERAL INFORMATION:
     APPLICANT: Bertin, John
     TITLE OF INVENTION: NOVEL MOLECULES OF THE / ARD-RELATED
     TITLE OF INVENTION: PROTEIN FAMILY AND USE: THEREOF
     FILE REFERENCE: 07334-076001
     CURRENT APPLICATION NUMBER- US/09/099,041A
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NUMBER OF SEQ ID NOS: 37
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US 09-099-041A-5
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         taunintaidennumennumenäss sägusessa
       1 TFLFAVIOLKETKLOSVSSAIHLCDKKEMELSLNIPVNHGPQEECGGSQLHENSGSPET 60
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, Sequence 6, Application US/09099041A
; Patent No. 6340576
; GENERAL INFORMATION:
: APPLICANT: Bertin, John
  TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD RELATED
   TITLE OF INVENTION. PROTEIN FAMILY AND USES THERE F
   FILE REFERENCE: 07334-076001
  CURRENT APPLICATION NUMBER, UC/09/099,041A
  CURRENT FILING DATE: 1998-06-17
   PRIOR APPLICATION NUMBER: 09/019.942
   PRIOR FILING DATE: 1998-02-06
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US-09-099-041A-6
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04
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         1 OPGIAQQWIQSKREDIVNOMTEACLMOSLDALLSRDLIMKEDYELVSTKPTRTSKVRQLL 6
Db
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: Sequence 25, Application 08/07857224B : Patent No. 5958784
  GENERAL INFORMATION:
    APPLICANT: Benner, Steven A.
    TITLE OF INVENTION: Predicting Folded Structures of iroteins
    NUMBER OF SEQUENCES: 114
    CORRESPONDENCE ADDRESS:
      ADDRESSEE: Steven A. Benner
      STREET: Hadlaubstrasse 151
      CITY: Zurich
      STATE: none
      COUNTRY: Switzerland
      ZIP: (note: this is an international post code) "E-me92
    COMPUTER READABLE FORM:
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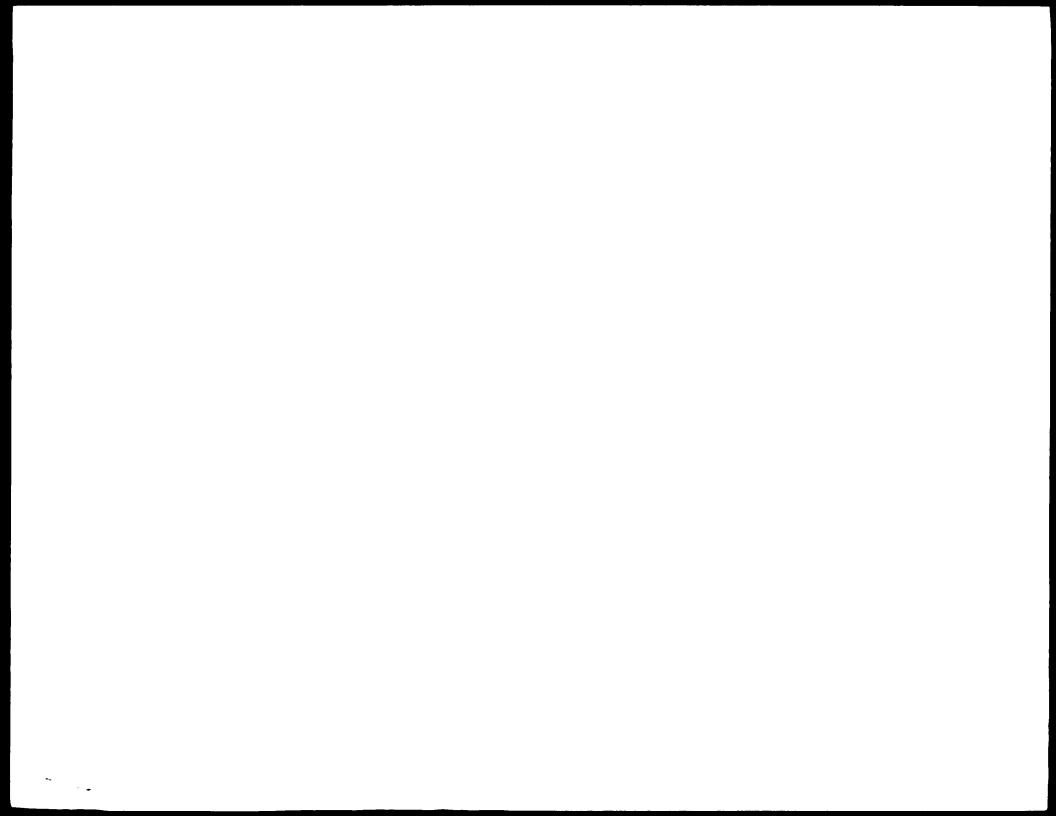
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        OPERATING SYSTEM: MacIntosh 7.0
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        APPLICATION NUMBER 115,007, 857, 224B
        FILING DATE: 03/25/92
        CLASSIFICATION: 436
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        TELEPHONE. (International) 41 1 632 2830
        TELEFAX: (international) 41 1 262 2437
        TELEX: none
    INFORMATION FOR SEQ ID NO: 25:
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        LENGTH: 257
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      ORIGINAL SOURCE:
       ORGANISM: Saccharomyces cerevisiae
      FEATURE: Protein kinase: Table 8 Column 18
      PUBLICATION INFORMATION:
        AUTHORS:
        AUTHORS: Hanks, S. K
       AUTHORS: Quinn, A. M.
AUTHORS: Hunter, T.
       TITLE: The protein kinase family
       JOURNAL: Science
       VOLUME: 241
       PAGES: 42-52
       DATE: 1988
US-07-857-2248-25
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; Sequence 30, Application Us/08701191A
 Patent No. 5442426
  GENERAL INFORMATION:
    APPLICANT: Mocsa Mohammadi, Joseph Schlessinger,
    APPLICANT: and Stevan R. Hubbard
    TITLE OF INVENTION: CRYSTALS OF THE TYROSINE KINASE DOMAIN
    NUMBER OF SEQUENCES: 41
    CORRESPONDENCE ADDRESS:
      ADDRESSEE: Lyon & Lyon
      STREET: 633 West Fifth Street
      STREET: Suite 4700
     CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
      ZIP: 90071-2366
    COMPUTER REALABLE FORM:
     MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
      MEDIUM TYPE: storage
     COMPUTER: IBM Compatible OPERATING SYSTEM: IBM P.C. DOS 5.0
     SOFTWARE: FastSEQ for Windows 2.0
   CURRENT APPLICATION DATA:
     PRLICATION NUMBER: US/08/701,191A
          DATE: August 21, 1996
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PRIOR APPLICATION DATA:
          APPLICATION NUMBER:
          FILING DATE:
        ATTORNEY AGENT INFORMATION:
          NAME: Warburg, Richard J.
          REGISTRATION NUMBER: 32,327
          REPERENCE/DOCKET NUMBER: 027/088
        TELECOMMUNICATION INFORMATION:
         TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
          TELEX: 67-3510
      INFORMATION FOR SEQ TO NO: 30:
       SEQUENCE CHARACTERISTICS:
         LENGTH: 304 amino acids
          TYPE: amino acid
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 : Sequence 2. Application PC/TUS9508493
    GENERAL INFORMATION:
      APPLICANT: Wood, Clive
      APPLICANT: Caruso, Anthony
TITLE OF INVENTION: Novel mik Receptor Typesing Einapop
      CORRESPONDENCE ADDRESS:
        ADDRESSEE: LEGAL AFFAIRS
        STREET: 87 CambridgePark Drive
        CITY: Cambridge
        STATE: MA
        COUNTRY: USA
        ZIP: 02140
      COMPUTER READABLE FORM:
        MEDIUM TYPE: Floppy disk
       COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS,MS DOS
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       FILING DATE:
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     ATTORNEY/AGENT INFORMATION:
       NAME: Brown, Scott A
       REGISTRATION NUMBER: 32,724
       REFERENCE/DOCKET NUMBER: GI5234A
     TELECOMMUNICATION INFORMATION:
       TELEPHONE: (617) 498-8224
       TELEFAX: (617) 876-5851
   INFORMATION FOR SEQ ID NO: 2:
     SEQUENCE CHARACTERISTICS:
      LENGTH: 530 amino acids
      TYPE: amino acid
      TOPOLOGY: linear
    MOLECULE TYPE: protein
PCT-US95-08493-2
 Query Match
 Ouery Match

1.7%; Score 9; DB 5; Length 530;

Best Local Similarity 100 0%; Prod No. 1
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GenCore version ..5
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OM protein - protein search, using sw model
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               6: Kojnžje je odataji, saujbackfilost poj *
     Pred. Not is the number of results precipted by chance to have a
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score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARTES

Result		Query				
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7	284	52.6	284	4	US-09-069-013-5	Sequence 5, Appli
8	221	4 (1 %	366	4	H-A1 -0-90-09-09	Sequence 4, Appli
9	195	+6.1	264	4	US-09-069-0:3-7	Sequence 7, Appli
10	167	. 11 G	167	4	##\$-09-969-## £	≲equence €, Appli
1.1	111	20.6	131	4	US-09-099-0/1A-5	Sequence 5, Appli
1.2	1004	20.0	1	4	778-09-099 D 18 6	Σequence €, Δ[jd]
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14	9	1.7	3 🗆 4	2	ne 00 aul - 11V 30	Sequence 30, April
15	Ġ	1.7	530	5	PCT-US95-08-93-2	Sequence 2, Appli
16	9	1.7	633	4	US-08-557-0-60-43	Sequence 43, Appl
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19	4	i _a	946	2	THR CH 003 204 12	Sequence 12, April
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20		1 7	860	۲,	PCT ।।दव5ः तमः वरः १०	Sequence 19, Appl
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10	٠.	1 7	સરક	2	198 - 198 - CA4 (2011)	fequence 1, App 11
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4 0	9	1.7	1082	1	US-08-457-598-S	Sequence 5, Appli
+1	9	1.7	1082	l	US-08-357-598-10	Sequence 10, Appl
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ALIGNMENTS

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RESULT 1
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; Patent No. 634857+
; GENERAL INFORMATION:
; APPLICANT: Numez, Gabriel
APPLICANT: Inohara, Nachiro
APPLICANT: Inohara, Nachiro
APPLICANT: Koscki, Takeyishi
Tifle of Invention of messic os AND METHOD FOR CONTINUEYING APOPLOSIS
THEE OF INVENTION OF THEALTH FATHWAY INSPECTORS ONS ACTIVATORS
  FIGUREFERENCE: UM 02233
    WELDT BIRTON, IN NUMBER 10, 54 OF 9, 923A
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; NUMBER OF SEQ ID NOS: 38
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; SEQ ID NO 4
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LL
     140 PPILIHEDERTONIERDNEFHVRIADEGESKWRMMSESOSESKSAPEGGTITYMPPENYP 199
27
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Lib
     200 FORESEAS FERD LYSYAVITWEVLSEKOPPEDVINES OF MYSVSCHIEPVINESS PYD 1 259
        Db
     139 POTESEAGIERITY.YAVITWEVILIEK PPETATROL (MYSVY) PIESVINESLEYDI 197
     200 PHRAEMEDICESCWACHPDERFOTERCLIELEPVERSEEDIFLEAVIQUER FEIGSVSS 319
        Tye Tarkarminininggwachitneringegninnen vielfennitetenviljnetelelogvys 257
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ÚΥ
        ra.
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44 ( 1, 3KRED: VNGMEDACENQCERALIDING LIMBER BEVSEKELKESKVROLLDE DEGAL 499
                       878 T. SKERDI VNOM DA DINGUDIANI DESTINARI PILIVETRE LE DEVEGUINI I. 10 d. 4-7.
               500 EFAKVIVCKERONEOM JOONEEL VYLEJANJAN LONKOM 549.
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               A ON FRANCING RUBE BROWN CONTRACTOR IN THE CARLOTTER
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     Sequence - Application USZSSERGOCKA
     Patient No. + 485 13
    GENERAL INCORMATION:
       APPLICANT Numer, Gabriel
       APPLICANT Inchira, Nachiro
       APPELICANI Koseki, Takeyoshi
       TITLE OF INVENTION. COMESSITIONS AND METHODS FOR IDENTIFYING APOPTABLE
       TIFLE OF INVENTION, SIGNALING PAIRWAY INBIBLIORS AND ACTIVATORS
       FILE REFERENCE, OM OTTOTAL
       CUPPENT APPLICATION NUMBER: US/03/06/3,023A
       CURRENT ELLING DATE: 1998 04 27
       NUMBER OF SEQUENCES RESERVED
       SOFTWARE Catentin Very 2.5
     SEQUENCE:
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    HS.18. (School 161. SR 4) Length 530.

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              4.10 TQL KEED IANQMEDACINGSEDALESSELLIMKESYEDVSEKPERTSKVROLLDTTD FOGE 499
                       4 to TeckREDIVNOMIBACINGSEDALECRELIMBLEVELVSIKHTRIBKVROLERITERGÖR, 4 cc.
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   Sequence 1 Appl. ation USZ090690, 3A
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, APPLICANT, Numez, Gabriel
; APPLICANT: Inohara, Nachiro
       Airth DAMI, Boacki, Take, oshi
       TITLE OF INVENTION, COMPOSITIONS AND METHODS FOR IDENTIFYING APOPTOSIS
       TITLE OF INVENTIONS FIGUREING PATHWAY UNHIBITORS AND ACTIVATORS
       FILE REFERENCE: UM=03333
         J. FELMI, Al Phys. CA. J. N. N. MRDEL, 1987 (1987) 0697 023A.
       CHRRENT FILING DATE: 1998-04-27
       NUMBER OF SECTIONOS: 48
       SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 1
        LENGIH: 531
        TYPE: PRT
       ORGANISM: Homo sapiens
US 09 069-023-1
                                                           85.4%; Score 461; DB 4; Length 531;
    gaery Match
    Best Local Similarity 100.0%; Pred. No. 0;
    Matches 461, Conseivative 0, Mismatches
                                                                                                                  0, Indels 0, Gaps
                80 PILGICNEPEFLGIVTEYMPNGSLNELLHRKTEYPDVAWELRFRILHEIALGVNYLHNMT 130
                      71 FILGTONESSING OVERWENGS ENELLERKTING DVANGERERALGVNYLHNMT 130
District
              140 PPLLBHOLKTONTILIONERHYKTADEGLSKWRMMSLSOSKSSKSAPROGITTYMPPENYE 199
                      131 PPELBHDIKTONTELDNEHVKTADEGESKWRMMSLSUSKSSKSAPEGGITTYMPPENYE 190
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               200 PGCKSRASTKHDTYSYAVTTWEVLSRKOPFEDVTNPLGTMYSVSQGHRDVTNEESLDYDT 259
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                       191 POOKSKADIKHDIYSYAVITWEVESKKOPPEEVINPLOIMYSVSOSHKEVINEESLEPIS 250
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                       37 Г. НУЕМЕЦИИЛЕОВИКИЕСТ ГУЗУДЖАВУОНКОЕ РОЗЗА СРВОТОВАЛЬТЕМ ДОСТАДОМ. 4 3 О.
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: 1
RESHLT 4
US 09 069 023-27
: Sequence 27, Application US/0906902:A
   Patent No. 6348573
; GENERAL INFORMATION:
; APPLICANT: Numez, Gabriel
      APPLICANT: Inohara, Nachiro
; APPERMANT: Koseki, Takeyoshi
; TILLE OF INVENTION, COMPOSITIONS AND METHODS FOR HENTIFYING APOPTOSIS
       TITLE OF INVENTION: SIGNALING PATHWAY INHIBITED AND ACTIVATORS
     FILE REFERENCE: UM-03333
       COMMENT APPLICATE NOT MEDICAL TO A MEDICAL TO A STATE OF THE A STA
     CURRENT FILING DATE: 1998-04-27
      NUMBER OF SEC ID NOS: 38
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 27
: LENGTH: 540
        TYPE: PRI
        ORGANISM: Homo sapiens
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HS-09-069-023-27

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Unery Match 85.4%; Score 461; DB 4; Length 540; Best Local Similarity 100.0%; Pred. No. (;
        Matches 461; Conservative 0; Mismatches
                                                                                                                                                                                                                              0; Indels 0; Gaps
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                                            80 PILGICNEPEFLGIVTEYMPNGSLNELLHRKTEYPIVAWPLRFRILHEJALGVNYLHNMI 139
                            140 PPLLHHDLKTONILLDNEFHVKIADEG SKWRMMS SOSKSSKSAPEGGIIIYMEPENYE 199
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                            380 CYPMKLHECPONBSWIFTISOSORAAFOHKTTPCISALINTISTAGNSERLOPGLACOW 439
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RESULT 5
US:09:014:442-1
: Sequence 1, Application US/09019942
 : Patient Mr. ការ៉ាក់កាត
 : GENERAL INFORMATION:
                     APPLICANT. Bertin, John
                      TITLE OF INVENTION: GENES ENCODING CASPASE RECRUITMENT
                       TITLE OF INVENTION: DOMAIN POLYPEPTIDES
                      NUMBER OF SEQUENCES: 4
                      CORRESPONDENCE ADDRESS:
                              ADDRESSEE. Fish & Richardson P.C. STREET: 225 Franklin Street
                               Cliy: Boston
                              STATE: MA
                              COUNTRY: USA
ZIP: 02110 2804
                      COMPUTER READABLE FORM:
                              MEDIUM TYPE. Diskette
                              COMPUTER: IBM Compatible
                               OPERATING SYSTEM Windows of
                               SOFTWARE: FastSEQ for Windows Versior 2.0b
                      CURRENT APPLICATION DATA:
                               APPLICATION NUMBER: US/09/019,942
                               FILING DATE: 06-FEB-1998
                      PRIOR APPLICATION DATA:
                               APPLICATION NUMBER:
                               FILING DATE:
                      ATTORNEY/AGENT INFORMATION:
                               NAME: Meiklejohn, Ph.D., Amita L.
                               REGISTRATION NUMBER: 35,283
REFERENCE THOMPSE 1073-4,068001
                       TELECOMMUNICATION INFORMATION.
                              TELEPHONE: 617/542-5070
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TELEFAX: 617/542-8906
                              TELEX: 200154
             INFORMATION FOR SEC 10 Not 1:
                    SEQUENCE CHARACIERISTICS:
                             LENGTH: 540 amino acids
                              TYPE: amino acid
                              TOPOLOGY: linear
                    MOLECULE TYPE, protein
 JS-09-019-942-1
       Query Match 66.7\%, Score 860; DB 3; Length 540; Best Local Similarity 99.8\%; Prod. No. 0; Matcher 460; Conservative 0; Mismatches 1; Ledels
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 RESULT 6
US-09-099 041A 2
 ; sequence 2, Application Us/09099041A
 : Patent No. 6340576
 ; GENERAL INFORMATION:
         APPLICANT: Bertin, John
            TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED
            TITLE OF INVENTION. PROTEIN FAMILY AND USES THEREOF
         FILE REFERENCE: 07 (34-076001
            CURRENT AFFERDATI & NUMBER, US/CO/USO, 041A
            CURRENT FILING DAIL: 1998-06-17
            FRIDE APELITATION NUMBER: 05,7019,942
           PRIOR FILING DATE: 1:98-02-06
            NUMBER OF SEC ID NOS: 37
           SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO 2
           LENGTH: 540
                TVPF: PRT
               ORGANISM: Homo sapiens
 US-09:099 041A 2
                                                                                                             .64.7%; Srove 360; DB 4; Length 540;
         energy Motobs
         Best local Similarity 99.8%; Pred. No. 0;
         Matches 460, Comperinative 6, Mismatches 1: Indels 0; Gaps
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                      140 PO CLUBBLEKTONTERENRETBYKTARPOLIKKWEMMSLEGGSESSKSAPEGGTITYMIPPENYE 199
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    Sequence ( Appl. sation US/0000062 A
    Patient No. 5348513
     CENERAL IN TEMAL . - N .
      APPLICANT Numeric Clabriel.
       APPLACANT Inchara, Nachira
       APPOJCANI Koseko. Lakeyosta
       TITLE OF INVENTOR OF MERCOLD ME ALLO MEDICAL FOR FORMATTY AND APPEARAGE
       TITLE OF INVENTIONS SIGNALING PAIRWAY INHIBITORS AND ACTIVATORS
       FILLE NEEDELENATE, OM 2004 03
       STURRENT A FILETA ION NUMBERS USZOSZOCS, OLSA
       STORRERY For LING LATE: 1998 04 27
       NUMBER OF BUILDINGS 38.
       200E (WARE: Patentin Ver. 2.0)
     DESCRIPTION
        1.000 01 41: 3, 94:
          TYEE . PE
          ROTANISM From Carptons
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                                                    52.6%; Score 284; DB 4; Length 284;
    Fest Forai Commission 100.0%; ered, No. 4,6e 279;
    Matches 204: Conservative 0; Mismatches 0; Indels 0; Gaps
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              3370 VS: 5191-2 PKKMP1 SENTEVNIEDE, DESSAS SEGERENSESERETERSERARGENBELSEK. 276
                      3.1. VB ACHIETEREREITENTEVNETEGELIG VICEGERRANDEREITEREITEREITERE 125
              377 AQ: "YEMKLUHCPONHSWDSTESGSQRAAFCDHKTTPCSSATINFLSTAGNSERLOFGTA 436
                      T. I AC. TYPMKERRICHSNESKER ERSSCHAAFCHIKELFESSAFINELSTAGNSERLOPTIA 180
              4.57 pcw., TKPE IVNEMIEACTNESDAGESRDUMKERYEDVSIKERRISKVROIDDIIIDI 4.96
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Db
           181 QQWTQSKREFTVNQMTEATENQSEFALESRETTMKEFYETVTTKFFRTSKVRQLLDTTDI 240
           157 JUNEPARVIVER FOREQUEU GOVERN VVOECE SENELENKON 540
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                  241 OCEREARVIVORERENROMENCOPYPETEVVORCESENDECINESM 284
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RESIDET 8
US:09 099-041A 4
; Sequence 4, Application US/09099041A
; Patent No. 6340576
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARL RELATED
. THILE OF INVENTION: TROTTED FAMILY AND USES THEREOF
; FILE REFERENCE: 07434 076001
     CORREST ARTICATION NUMBER 103,703,7730,041A
: CURRENT FILING DATE: 1998 06:17
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: PRIOR FILING DATE: 1998:02 06
, NUMBER OF SEC ID NOS: 47
     SOFTWARE: FastSEQ for Windows Version 4.0
: SEQ 10 NO 4
: LENGTH: 400
      TYPE: PRI
     ORGANISM: Homo sapiens
US-09-099-041A-4
   Ouery Match 40.9%; Score 221; DB 4; Length 800; Bost (real Similarity 100.0%; Pred. No. 2.5e 215;
   Matches 221; Conservative 0; Mismatches 0; Indels 0; Gaps
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           110 PPELHHDEKTONIELDNECHVKTADEGECKWRMMSESGGEGGKSAPEGGTTTYMFPENYE 199
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                  200 PGOKSKASTKHDTYSYAVTTWEVLSRKOPPEDVINDLGTMYSVSGGBREVTNEESLPYDT 21/04
i.b.
           260 PHRARMISLIESCWAUNPDERPSFLECLIEDEPVERTFELL 300
                 260 PHRARMISLIESGWAQNPDERPSFLKCLIELEPVLRTFEEL 300
RESULI 9
US:09 069:023:7
; Sequence 7, Application US/09069023A
; Patent No. 6348573
J GENERAL INFORMATION:
; APPLICANT: Numez, Gabriel
; APPLICANT: Inohara, Nachiro
; APPLICANT: Koseki, Takeyoshi
: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR HENTIFYING APOPTOSIS
    TITLE OF INVENTION, BIGNALING LATHWAY INSIBIL SO AND ACTIVATORS
; FILE REFERENCE: UM-03333
       TISEENI APPLICATIEN NOMPEE TIJOS,069,023A
 ; CURRENT FILING DATE: 1998-04-27
     NUMBER OF SEQ ID NOS: 38
    SOFTWARE: PatentIn Ver. 2.0
; SEQ 10 NO 7
; 1.ENGTH: 264
      TYPE: PRT
     ORCANISM: Homo sapiens
05:09 069 023-7
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Query Motch 36.1%; Score 195; DR 4; Length 264; Best Local Similarity 100.0%; Pred. No. 4.3e-189;
   Matches 195; Conservative 0; Mismatches 0; Indels 0; Gaps
            80 PHIGIONEPERIGIVTEYMPNGSLNELLHRKTEYFDVAWPLRFRILHEIALGVNYLHNMT 139
                  1.5 - 1.5 | 4 | 1.5 | 5 | 5 | 5 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1
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           140 PETERHOLKTONIII DNEFEVKIADECLSKWEMMSLSOSESSKSAPECCTIIYMEEENYE 199
07
                 Βb
           130 PFLLHHELKTQNILLDNEFHVKIADFGLSKWRMMSLSQSRSSKSAPEGGTTIYMPPENYE 189
           ZUO POCKSRASIEBDIYSYAVIIWEVLSREQPEEDVINDDJMYSVSQOHROVINERSLPYDI 259
UV
                190 PGQKSRASIKHDIYSYAVITWEVLSRKQPFEDVT1PLQIMYSVSQCHRPVINEESLPYDI 249
Db
           260 PHEARMISLIESGWA 274
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RESHLT 10
US-09-069-023-6
: Sequence 6, Application US/09069023A
; Patent No. 6348573
: GENERAL INFORMATION:
; APPLICANT: Numez, Cabriel
    APPLICANI: Inchara, Nachiro
    APFLICANT, Köseki, Takeyoshi
     TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR IDENTITYING APOPTOSIS
    TITLE OF INVENTION, SIGNALING PAIRWAY INH BITORS AND ACTIVATORS
    FILE REFERENCE: UM-03333
    CUPRENT APPLICATION NUMBER, US, US, US, US, CES, CES, CURRENT FILLING PATE: 1998 04 27
    NUMBER OF SEQ ID NOS: 38
    SOFTWARE: Patentin Ver. 2.0
   SEQ ID NO 6
    LENGTH: 167
      TYPE: PRT
      ORGANISM: Hono sapiens
08-09-069-023-6
   Query Match
                                             30.9%; Score 167; DB 4; Length 167;
   Best Local Similarity 100.0%: Pred. No. 5.8e-161;
Matches 162 Conservation 0, Mismatthe. 0, Indexs 0, days
           374 SPRAQDOYEMKI.HHOPONHSWDSITSOSQRAAPOTHKTTPOSSATINPISTAGNSERLQP 433
QY
                 1 SRKAODCYFMKLHHCPGNHSWDSTISGSORAAFCOHKTTPCSSAlinpLSTAGNSERLOP 60
           434 GIAQQWIQSKREDIVNQMTEACLNQSLDALLSRCJIMKEDYELVSTKPTRTSKVRQLLDT 493
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                 Db
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UST
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          Db
RESULT 11
US-09-099-041A-5
   Sequence 5, Application US/09099041A
   Patient No. 6340576
   GENERAL INFORMATION:
   APPLICANT: Bertin, John
    TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD RELATED
     TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF
     FILE REFERENCE: 07334-076001
     CURRENT APPLICATION NUMBER: US/09/099,041A
     CURRENT FILING DATE: 1998-06-17
    PRIOR APPLICATION NUMBER: 09/019,942
    PRIOR FILING DATE: 1998 02 06
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NUMBER OF SEC ID NOSE 37
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 ; SEO ID NO 5
           LENGTH: 131
            TYPE: PRT
           ORGANISM: Homo sapiens
US-09-099-041A-5
      Query Match 20.6%: Score 111: 18 4: Length 131: Best Local Similarity 100.0%; Pred. No. 20:104:
       Matches III; Conservative 0; Mismatches 0; Indels 0; Gaps
                    30] IEPEAVIOREK ELOGVOGATHIOTEKERMOLELNIDVARD CORPOTEDOS HENSGSPET 360
                              1 PPLEAVIOLEKIKLOSYSSA (BLODEKEMBLSLN) PVNHGPQBDSCGSSQLHENSGSPET 60
Ob
                    361 SPYTPAPCENTERING ACTION ACTIONS TO THE SWELTT SOSCENAR TORKE 411
OV
                     THTHEFT HILLITE HILLITE HILLITE HILLITE HILLITE HILLITE HILLITE HILLITE HILLITE HILLITE HILLITE HILLITE HILLITE HILLITE HILLITE HILLITE HILLITE HILLITE HILLITE HILLITE HILLITE HILLITE HILLITE HILLITE HILLITE HILLITE HILLITE HILLITE HILLITE HILLITE HILLITE HILLITE HILLITE HILLITE HILLITE HILLITE HILLITE HILLITE HILLITE HILLITE HILLITE HILLITE HILLITE HILLITE HILLITE HILLITE HILLITE HILLITE HILLITE HILLITE HILLITE HILLITE HILLITE HILLITE HILLITE HILLITE HILLITE HILLITE HILLITE HILLITE HILLITE HILLITE HILLITE HILLITE HILLITE HILLITE HILLITE HILLITE HILLITE HILLITE HILLITE HILLITE HILLITE HILLITE HILLITE HILLITE HILLITE HILLITE HILLITE HILLITE HILLITE HILLITE HILLITE HILLITE HILLITE HILLITE HILLITE HILLITE HILLITE HILLITE HILLITE HILLITE HILLITE HILLITE HILLITE HILLITE HILLITE HILLITE HILLITE HILLITE HILLITE HILLITE HILLITE HILLITE HILLITE HILLITE HILLITE HILLITE HILLITE HILLITE HILLITE HILLITE HILLITE HILLITE HILLITE HILLITE HILLITE HILLITE HILLITE HILLITE HILLITE HILLITE HILLITE HILLITE HILLITE HILLITE HILLITE HILLITE HILLITE HILLITE HILLITE HILLITE HILLITE HILLITE HILLITE HILLITE HILLITE HILLITE HILLITE HILLITE HILLITE HILLITE HILLITE HILLITE HILLITE HILLITE HILLITE HILLITE HILLITE HILLITE HILLITE HILLITE HILLITE HILLITE HILLITE HILLITE HILLITE HILLITE HILLITE HILLITE HILLITE HILLITE HILLITE HILLITE HILLITE HILLITE HILLITE HILLITE HILLITE HILLITE HILLITE HILLITE HILLITE HILLITE HILLITE HILLITE HILLITE HILLITE HILLITE HILLITE HILLITE HILLITE HILLITE HILLITE HILLITE HILLITE HILLITE HILLITE HILLITE HILLITE HILLITE HILLITE HILLITE HILLITE HILLITE HILLITE HILLITE HILLITE HILLITE HILLITE HILLITE HILLITE HILLITE HILLITE HILLITE HILLITE HILLITE HILLITE HILLITE HILLITE HILLITE HILLITE HILLITE HILLITE HILLITE HILLITE HILLITE HILLITE HILLITE HILLITE HILLITE HILLITE HILLITE HILLITE HILLITE HILLITE HILLITE HILLITE HILLITE HILLITE HILLITE HILLITE HILLITE HILLITE HILLITE HILLITE HILLITE HILLITE HILLITE HILLITE HILLITE HILLITE HILLITE HILLITE HILLITE HILLITE HILLITE HILLITE HILLITE HILLITE HILLITE HILLITE HILLITE HILLITE HILLIT
Oto
 RESULT 12
US-09-099-041A-6
 : Sequence 6, Application US/09099041A : Patent No. 6340576
 ; CENERAL INFORMATION:
 ; APPLICANT: Bertin, John
  , TITLE OF INVENTION, NOVEL MOLECULES OF THE CARD RELATED
         TITLE OF INVENTION. FROHER PAMILY AND USES THEREOF
 ; FILE REFERENCE: 07+34-076001
  ; CURRENT APPLICATION NUMBER: US/109/099,041A
         CURRENT FILING DATE: 1998 06 17
         PRIOR ALFIJICATION NUMBER: 00/019,942
         PRIOR FILING DATE: 1998-02-06
         NUMBER OF SEQ ID NOSE 37.
         SOFTWARE: FastSEQ for Windows Version 4.0
  · SEO ID NO 6
 ; LENGIH: 109
             TYPE: PRT
            ORGANISM: Homo sapiens
 US-09-099 041A-6
      Query Match 20.2%; Score 109; DB 4: Length 109: Rest Letal Similarly, 1...el. Fred. No. 1.8e-102; Matches 109; Conservative 0: Mismatches 0: Indels
                   432 OPCIACOWIOSERFEITVNOMTFACINOSIDATISEDCIMEEDYFIVSIEPTETSEVECLL 491
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                         THE HALL HAS DEFINED BY A THE FOREIGN SHOWN SHOWS THE HALL HAS BEEN AND A SHOW THE FOREIGN SHOWS AND A SHOW THE SHOW THE SHOW THE SHOWS AND A SHOW THE SHOW THE SHOWS AND A SHOW THE SHOWS AND A SHOW THE SHOWS AND A SHOW THE SHOWS AND A SHOW THE SHOWS AND A SHOW THE SHOWS AND A SHOW THE SHOWS AND A SHOW THE SHOWS AND A SHOW THE SHOWS AND A SHOW THE SHOWS AND A SHOW THE SHOWS AND A SHOW THE SHOW THE SHOW THE SHOWS AND A SHOW THE SHOW THE SHOW THE SHOW THE SHOW THE SHOW THE SHOW THE SHOW THE SHOW THE SHOW THE SHOW THE SHOW THE SHOW THE SHOW THE SHOW THE SHOW THE SHOW THE SHOW THE SHOW THE SHOW THE SHOW THE SHOW THE SHOW THE SHOW THE SHOW THE SHOW THE SHOW THE SHOW THE SHOW THE SHOW THE SHOW THE SHOW THE SHOW THE SHOW THE SHOW THE SHOW THE SHOW THE SHOW THE SHOW THE SHOW THE SHOW THE SHOW THE SHOW THE SHOW THE SHOW THE SHOW THE SHOW THE SHOW THE SHOW THE SHOW THE SHOW THE SHOW THE SHOW THE SHOW THE SHOW THE SHOW THE SHOW THE SHOW THE SHOW THE SHOW THE SHOW THE SHOW THE SHOW THE SHOW THE SHOW THE SHOW THE SHOW THE SHOW THE SHOW THE SHOW THE SHOW THE SHOW THE SHOW THE SHOW THE SHOW THE SHOW THE SHOW THE SHOW THE SHOW THE SHOW THE SHOW THE SHOW THE SHOW THE SHOW THE SHOW THE SHOW THE SHOW THE SHOW THE SHOW THE SHOW THE SHOW THE SHOW THE SHOW THE SHOW THE SHOW THE SHOW THE SHOW THE SHOW THE SHOW THE SHOW THE SHOW THE SHOW THE SHOW THE SHOW THE SHOW THE SHOW THE SHOW THE SHOW THE SHOW THE SHOW THE SHOW THE SHOW THE SHOW THE SHOW THE SHOW THE SHOW THE SHOW THE SHOW THE SHOW THE SHOW THE SHOW THE SHOW THE SHOW THE SHOW THE SHOW THE SHOW THE SHOW THE SHOW THE SHOW THE SHOW THE SHOW THE SHOW THE SHOW THE SHOW THE SHOW THE SHOW THE SHOW THE SHOW THE SHOW THE SHOW THE SHOW THE SHOW THE SHOW THE SHOW THE SHOW THE SHOW THE SHOW THE SHOW THE SHOW THE SHOW THE SHOW THE SHOW THE SHOW THE SHOW THE SHOW THE SHOW THE SHOW THE SHOW THE SHOW THE SHOW THE SHOW THE SHOW THE SHOW THE SHOW THE SHOW THE SHOW THE SHOW THE SHOW THE SHOW THE SHOW THE SHOW THE SHOW THE SHOW THE SHOW THE SHOW THE SHOW THE SHOW THE SHOW THE SHOW THE SHOW THE SHOW 
Db
                    490 PRITETOCHERAKY (VOY) KENKOMEN ORYPETT VVEHSEST NY LONKSM-540.
                     BESULT 18
US-07-857 2248-25
 ; Sequence 25, Application 98/078572248
 ; Patent No. 5958784
 ; GENERAL INFORMATION:
               APPLICANT: Benner, Steven A.
                TITLE OF INVENTION: Predicting Folded Structures of Proteins
                NUMBER OF SEQUENCES: 114
                CORRESPONDENCE ADDRESS:
                     ADDRESSEE: Steven A. Benner
                      STREET: Hadlaubstrasse 151
                     CITY: Zurich
                     STATE: none
                     COUNTRY: Switzerland
                      Zir: (note: this is an international post code) CH:8092
                COMPUTER READABLE FORM:
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MEDI M TYPE - 3.5 inch diskette. 1.4 Mb storage
       PAMPITER: Apple MacIntosh
       OPERALING SYSTEM: MacIntosh 7.0
       COPTWARE: Microsoft Word
      "JEREN: APELL 'ALLON DATA:
      TAPPEL TALLE N. NOMBOR. - BOLZO ZZOS CEREBE
ETERRET DATES - OBJECTOR
      CLASSIFICATION: 436
     PER OR APPLICATION DAIA. mome
     DIRCEMMENTATION INFORMATION:
       iELEcH NE: (International) 1: 1 632 2830
       TELECON: (International) 41 1 262 2137
       TELLEX fromes
   INFORMAT IN FOR SEQ ID-NOT 25:
    CONQUENCE MARASTERISTICS:
      LENG.H: 2^{i-i}
       TYPE __min_card
    ToPC SY: Incor.
MajadCU. E. TYPE:
      - DESCRIPTION: protein
     PERIOTINAL BOURGIES
      - PGANISM: Jaccharomyces cejevisiae.
    FrAtOR: Protein kinase: Lable 8 Column 28
    PUBLICATION INFORMATION:
       ANTH: RSE
       AUTHORS: Binks, S. K.
       AUTHORS Colon, A. M. AUTHORS, Houter, I.
       Till: The protein kinase family
      DOURNAL Entende
VOLUME 241
MAGE: 42 %2
       DATE THRE
9.1 07 857 2.18 25
 Matches 9. Conservative 0; Missatches 0; Indels 0; Gaps 0-
19 166 VELADEGIL: 168
         T. 13.1113.3
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FESUL:1 14
 SC08 TVL 1 (LA 30)
 Sequence - Application USZ 08701191A
  Patient No. 50424.8
  GENERAL INFORMATION:
    APPLICANT: Moosa Mohammadi, Joseph Schlessinger,
    APPENDANCE and Steven R Buld rd
    THILE OF INVENTION: CRYSTALS OF THE TYROSINE KINASE DOMAIN
    TITLE OF INVENTION: OF NON INSULAR RECEPTOR TYROSINE KINASE
    NUMBER E DESCRIPTION 11
     1 MEESE NUENCE ADDRESS:
      APDRESSEE: Lyon & Lyon.
       STREETS BKY West Fifth Street
       STREE : Suite 4700.
       MILY. . s Angeles
MATE Tallfornia
       FOUNTEY: U.S.A.
       JIP: 96071 2066
    COMPUTE: REALABLE FORM:
      MEDIUM TYPE | C.C. Diskette, 1 44 ME
MEDIUM TYPE | storage
       *** MPUIER: IBM Compatible
       PERA INDUSTRIAL TRANSPORT OF STATE
       PerTWheter FirstSEQ for Windows 2.5
     THEREBY APPLICATION DATA:
      APPLI ALLON NUMBER: 98,709,72 1.191A
      3 L IN SAIR Adjust 21, 1996
       15/88 F. MI NE 500
```

```
PRIOR APPLICATION DATA:
      APPLICATION NUMBER:
      FILING DATE:
;
     ATTORNEY/AGENT INFORMATION:
      NAME: Warburg, Richard J.
      REGISTRATION NUMBER: 32,327
      BOOK FOR NOTE TO FREE NOMERN 1 277 TORR
     TELECOMMUNICATION INFORMATION:
      TELEPHONE: (214) 489 1600
      IELEFAX: (213) 955-0440
      TELEX: 67 3510
: INFORMATION FOR SEC ID NO: 30:
    SEQUENCE CHARACTERISTICS:
      LENGIH: 304 amino acids
      TYPE: amino acid
      STRANDEDNESS: single
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    MOLECULE TYPE: protein
US-08 701-191A 30
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RESULT 15
PCT-US95 08493 2
; Sequence 2, Application PC/TUS9508493
; GENERAL INFORMATION:
    APPLICANT: Wood, Clive
    APPELICANT: Caruso, Anthony
     TITLE OF INVENTION: Novel mlk Receptor Type Fine Kinases
     NUMBER OF SEQUENCES: 21
     CORRESPONDENCE ADDRESS:
      ADDRESSEE: LEGAL AFFAIRS
      STREET: 87 CambridgePark Drive
      ClfY: Cambridge
      STATE: MA
      COUNTRY: USA
      ZIP: 02140
     COMPUTER READABLE FORM:
      MEDIUM TYPE: Floppy disk
      COMPUTER: IBM PC compatible
      OPERATING SYSTEM: PC DOS/MS DOS
      SOFTWARE: PatentIn Release #1.0, Version #1.25
    CURRENT APPLICATION DATA:
      APPLICATION NUMBER: PCTZUS95Z08493
      FILING DATE:
      CLASSIFICATION:
     ATTORNEY/AGENT INFORMATION:
      NAME: Brown, Scott A
      REGISTRATION NUMBER: 12,724
      REFERENCE/DOCKET_NUMBER: G15234A
    TELECOMMUNICATION INFORMATION:
      TELEPHONE: (617) 498 8224
      TELEFAX: (617) 876 5851
  INFORMATION FOR SEQ 10 NO: 2:
    SEQUENCE CHARACTERISTICS:
      LENGTH: 530 amino acids
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      TOPOLOGY: Linear
   MOLECULE TYPE: protein
Bir 0095 08493 2
                        -1.7%, Score 9, DB 5, Length 530;
  Best Local Similarity 100.0%; Pred. No. 1;
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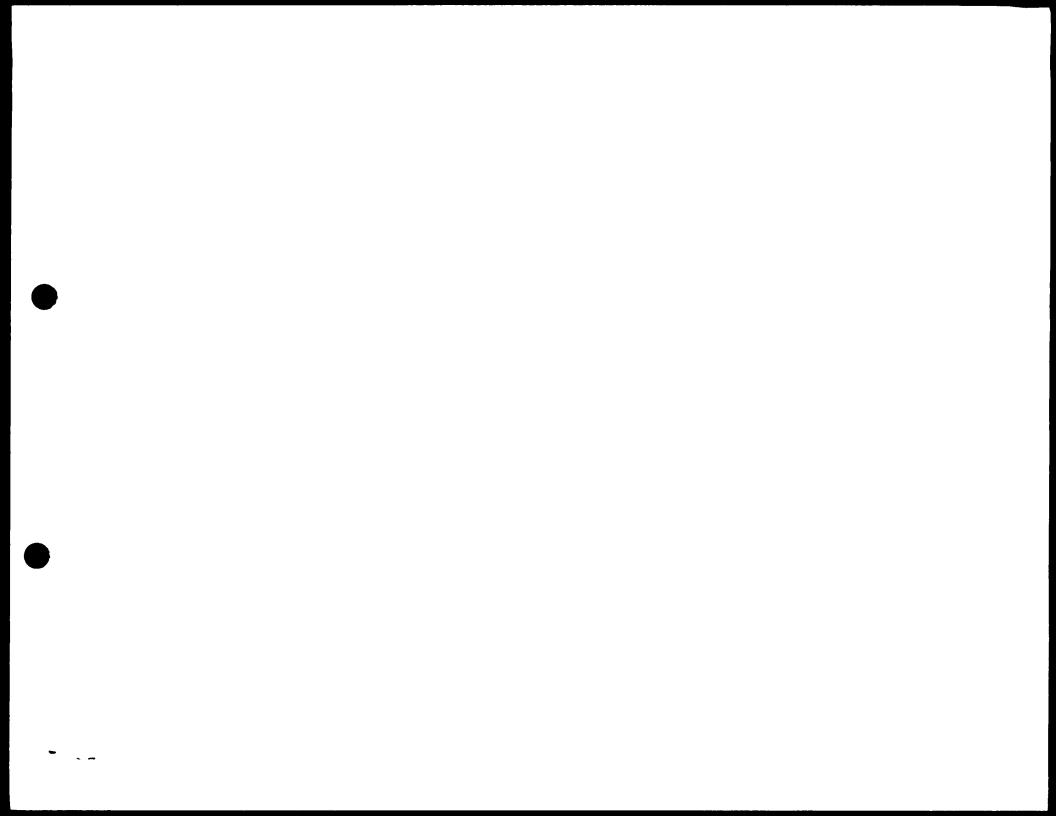
Search completed: May 13, 2002, 21:33:41 Job time: 5726 sec

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   09-069-023-6
; Sequence 6, Application US/09069023A; Patent No. 6348573
 GENERAL INFORMATION:
  APPLICANT: Nunez, Gabriel
  APPLICANT: Inohara, Naohiro
  APPLICANT: Koseki, Takeyoshi
  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR IDENTIFYING APOPTOSIS
  TITLE OF INVENTION: SIGNALING PATHWAY INHIB: ORS AND ACTIVATORS
  FILE REFERENCE: UM-03333
  CURRENT APPLICATION NUMBER: US/09/069,023A
CURRENT FILING DATE: 1998-04-27
  NUMBER OF SEQ ID NOS: 38
  SOFTWARE: Patentin Ver. 2.0
 SEQ ID NO 6
   LENGTH: 167
   TYPE: PRT
   ORGANISM: Homo sapiens
US-09-069-023-6
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                      30.9%; Score 167; D3 4; Length 167;
 Best Local Similarity 100.0%; Pred. No. 5.3e-161;
 Matches 167; Conservative
                           0: Mismatches
                                           0: Indels 0: Gaps
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US-09-099-041A-5
; Sequence 5, Application US/09099041A
; Patent No. 6340576
; GENERAL INFORMATION:
  APPLICANT: Bertin, John
  TITLE OF INVENTION: NOVEL MOLECULES OF THE (ARD-RELATED
  TITLE OF INVENTION: PROTEIN FAMILY AND USE: THEREOF
  FILE REFERENCE: 07334-076001
  CURRENT APPLICATION NUMBER USING JORG 041A
  CURRENT FILING DATE: 1998-06-17
  PRIOR APPLICATION NUMBER: 09/019,942
  PRIOR FILING DATE: 1998-02-06
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NUMBER OF SEQ ID NOS: 37
   SOFTWARE: FastSEQ for Windows Version 4.0
: SEO ID NO 5
   LENGTH: 131
   TYPE: PRT
   ORGANISM: Homo sapiens
US:09:099:041A 5
  Query Match 20.6%; Score 111; DR 4; Length 141; Best Local Similarity 100.00; Pred. No. 2e-104;
  Matches 111; Conservative 0; Mismatches
                                              0: Indets 0: Gaps
      301 TELEVATÓI KKIKI ÖSASSY I NI GOKKKWEI ALMI BANHADŐSBEGGGGGŐI HEMSÖSBEL (190
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Qv
          Db
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RESULT 12
US-09-099-041A-6
; Sequence 6, Application US/09099041A
 Patent No. 6340576
 GENERAL INFORMATION:
  APPLICANT: Bertin, John
   TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED
   TITLE OF INVENTION. FROTEIN FAMILY AND USES THEREOF
   FILE REFERENCE: 07+34-076001
   CURPENT APPLICATION NUMBER: US/09/099.041A
  CURRENT FILING DATE: 1998-06-17
   PRIOR APPLICATION NUMBER: 09/019,942
   PRIOR FILING DATE: 1998-02-06
   NUMBER OF SEQ ID NOS: 37
   SOFTWARE: FastSEQ for Windows Version 4.0
  SEO ID NO 6
   LENGTH: 109
   TYPE: PRT
   ORGANISM: Homo sapiens
US-09-099-041A-6
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017
      61 DITOTOGGEEFAKVIVQKI KINKOMI OFTEN LAVINGGEEGLANG GERM 109
Db
RESULT 13
US:07-857:224B-25
; Sequence 25, Application US/ 78572246
; Patent No. 5958784
GENERAL INFORMATION:
    APPLICANT: Benner, Steven A.
     TITLE OF INVENTION: Predicting Folded Structures of incleins
     NUMBER OF SEQUENCES: 114
    CORRESPONDENCE ADDRESS:
      ADDRESSEE: Steven A. Benner
      STREET: Hadlaubstrasse 151
      CITY: Zurich
      STATE: none
      COUNTRY: Switzerland
      ZIP: (note: this is an international post code) FB 8052
    COMPUTER READABLE FORM:
```

```
MEDIUM TYPE: 3.5 inch diskette, 1.4 Mb storage
             COMPUTER: Apple MacIntosh
OPERATING SYSTEM: MacIntosh 7.0
          SOFTWARE: Microsoft Word
CURRENT APPLICATION DATA:
             APPLICATION NUMBER US/07/852,224B
             CLASSIFICATION: 436
          PRIOR APPLICATION DATA: none
          TELECOMMUNICATION INFORMATION:
             TELEPHONE: (International) 41 1 632 2650
             TELEFAX: (International) 41 1 262 2437
      TELEX: none
INFORMATION FOR SEQ ID NO: 25:
          SEQUENCE CHARACTERISTICS:
LENGTH: 257
             TYPE: amino acid
            TOPOLOGY: linear
          MOLECULE TYPE:
            DESCRIPTION:
                                  protein
          ORIGINAL SOURCE:
            ORGANISM: Saccharomyces cerevisiae
         FEATURE: Protein kinase; Table 8 Column 23
         PUBLICATION INFORMATION:
            AUTHORS:
            AUTHORS: Hanks, 5. K.
          AUTHORS: Hanks, S. K.
AUTHORS: Quinn, A. M.
AUTHORS: Hunter, T.
TITLE: The protein kinase family
JOURNAL: Science
VOLUME: 241
PAGES: 42-52
DATE: 1586
857-2048-25
US-07-857-224B-25
   Ouery Match 1.7%; Score 9; DB 1; Length 257; Best Local Similarity 100.0%; Pred. No. 0 52;
                 9: Conservative
                                                   0; Mismatches 0; Indels
                                                                                                         0, Gaps
          160 VKTADEGLS 168
                A CONTRACTOR OF
         139 VKIADEGLS 147
RESULT 14
US-08-701-191A-30
  Sequence 30, Application US/08701191A Patent No. 5942428
    GENERAL INFORMATION:
       APPLICANT: Moosa Mohammadi, Joseph Schlessinger,
APPLICANT: and Stevan R. Hubbard
      APPLICANT: Moosa Mohammadi, Joseph Schlessinger,
APPLICANT: and Stevan R. Hubbaid
TITLE OF INVENTION: CRYSTALS OF THE TYPOSITE KINASE DOMAIN
NUMBER OF SEQUENCES 41
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY far Adminst
         CITY. Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
      COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
      MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5 0
SOFTWARE: FastSEQ for Windows 2.0
CURRENT APPLICATION DATA:
           PLICATION NUMBER: US/08/701,191A
DATE: August 21, 1996
SION: 530
```

```
PRIOR APPLICATION DATA:
             APPLICATION NUMBER:
              FILING DATE:
           ATTORNEY/AGENT INFORMATION:
             NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
              REFERENCE/DOCKET NUMBER: 227/088
           TELECOMMUNICATION INFORMATION:
             TELEPHONE: (213) 489-1600
TELEFAX: (213) 955 0440
TELEX: 67-3510
       TELEA: 67-3210
INFORMATION FOR SEQ 1D NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 304 amino acids
             TYPE: amino acid
             STRANDEDNESS: single
          TOPOLOGY: linear
MOLECULE TYPE: protein
  US-08-701-191A-30
     Query Match
Best Local Similarity 100 0%; Pred. No. 0.61;
     Matches 9: Conservative 0: Mismatches 0: Indels
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           160 VKIADFGLS 168
          RESULT 15
  PCT-US95-08493-2
   CT-US95-08493-2
Sequence 2, Application PC/TUS9508493
GENERAL INFORMATION:
APPLICANT: Wood, Clive
APPLICANT: Caruso, Anthony
TITLE OF INVENTION: Novel mlk Receptor Tyrosine Kinases
NUMBER OF SECUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: LEGAL AFFAIRS
           ADDRESSEE: LEGAL AFFAIRS
STREET: 87 CambridgePark Drive
           CITY: Cambridge
           STATE: MA
COUNTRY: USA
        ZIP: 02140
COMPUTER READABLE FORM:
          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM. PC-DOS/MS-DOS
           SOFTWARE: PatentIn Release #1.0, Version #1.25
        SOFTWARE: PALEHLLI ATTACHMENT APPLICATION DATA:
           FILING DATE:
           CLASSIFICATION:
        ATTORNEY/AGENT INFORMATION:
          NAME: Brown, Scott A
REGISTRATION NUMBER: 32,724
           REFERENCE DOCKET NUMBER: GIS234A
        TELECOMMUNICATION INFORMATION:
    TELECOMMUNICATION INFORMATION
TELEPHONE: (617) 498-8224
TELEFAX: (617) 876-5851
INFORMATION FOR SEO ID NO: 2:
       SEQUENCE CHARACTERISTICS:
          LENGTH: 530 amino acids
       TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US95-08493-2
  Query Match
  Ouery Match 1.7%; Score 9; DB 5; Length 530; Best Local Similarity 100 0%; Prod 9; 1
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GenCore version ..5
                                      Copyright (c) 1993 2000 Compagen Ltd.
 oM protein – proteis search, using sw model
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                                    May 17, 2002, 19.08.00 , Search time 122.31 Deconds
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                                    US-09-445-223-1
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 Word size :
Total number of hits satisfying chosen parameters:
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Minimum DB seq length: 0
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Database .
                                    A_Ceneseq 032802:*
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for these 00 (s1.6) yields a hell memosed years sequented, AA 1983 TAT *
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                                          ** AA1987 JAI: * * AA1989 AA1987 JAI: *
                                          *: PAU. 889 LAAN lide from the from the first the property of the first transfer that the first transfer the first transfer transfer that the first transfer transfer transfer transfer transfer transfer transfer transfer transfer transfer transfer transfer transfer transfer transfer transfer transfer transfer transfer transfer transfer transfer transfer transfer transfer transfer transfer transfer transfer transfer transfer transfer transfer transfer transfer transfer transfer transfer transfer transfer transfer transfer transfer transfer transfer transfer transfer transfer transfer transfer transfer transfer transfer transfer transfer transfer transfer transfer transfer transfer transfer transfer transfer transfer transfer transfer transfer transfer transfer transfer transfer transfer transfer transfer transfer transfer transfer transfer transfer transfer transfer transfer transfer transfer transfer transfer transfer transfer transfer transfer transfer transfer transfer transfer transfer transfer transfer transfer transfer transfer transfer transfer transfer transfer transfer transfer transfer transfer transfer transfer transfer transfer transfer transfer transfer transfer transfer transfer transfer transfer transfer transfer transfer transfer transfer transfer transfer transfer transfer transfer transfer transfer transfer transfer transfer transfer transfer transfer transfer transfer transfer transfer transfer transfer transfer transfer transfer transfer transfer transfer transfer transfer transfer transfer transfer transfer transfer transfer transfer transfer transfer transfer transfer transfer transfer transfer transfer transfer transfer transfer transfer transfer transfer transfer transfer transfer transfer transfer transfer transfer transfer transfer transfer transfer transfer transfer transfer transfer transfer transfer transfer transfer transfer transfer transfer transfer transfer transfer transfer transfer transfer transfer transfer transfer transfer transfer transfer transfer transfer transfer transfer
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Pred. No is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMAR ES

Result No.	score	* Ouery Match	Length	ЬВ	ID	Description
1	54	100.0	540	20	ΔΑ₩92795	Human Bl protein.
2	4 f 1	85.4	478	21	AAY59405	Human RICK protein
+	461	85.4	531	21	AAY59404	Human RICK protein
4	461	85.4	540	21	AAY68774	Amino acid sequenc
Γ,	461	85.4	544	21	AAB43570	Haman cancer assoc
F1	3 F. ()	66.7	540	20	AAY31140	Human CARD-3 prote
?	4.6.73	66.7	510	22	AAB20075	Homan CARD 3 prote
Н	_1H 1	C	.194	2.1	AAYEGIGE	Baran FICK pritein
(j	259	48.0	540	22	AAM93621	Human polypentide,
10	167	કેલ છ	167	2.1	ΑΛΥΕΘ405	Homan Pick picteli
1 1	126	21.1	153	21	AAB58938	Breast and ovarian

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                                                           Novel protein kina
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     AAW9, 795;
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    Homan Bl protein.
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    will surficil pathway intrabeltable signal deap AIDS; cancer; homan,
ХX
    Homo sapiens.
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                    9711.-0121746.
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     30 JUN 1997:
                    9711.-0121199.
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     Boldin M. Maliain N. Wallach D;
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    Wil. 1999 070256/06:
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    New El protein requiated cell death and cell survival pathways
    derivatives, DNA and antibodies, also regulate intracellular
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    anti-omation; for freating AIDS, cancer
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    This invention describes the isolation at a novel human 81 protein which
    can interact with, intracellular mediators or modulators of inflammation,
    cell death and/or cell survival pathways, directly or indirectly, Cells
     an to modelated or mediated in inflammation, cell death or cell survival
    pathways or another intracellular signalling activity using BL.
     fond to as such as Alles and stancer can be treated using Bl. Antibodies,
    dig notice tides and ribodymes can also be used to regulate the above
    pathways:
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     Gestur Leter 40 AA:
 query Match. | Dec.e%, Score 540; DB 20; Length 540; Best Book, Similarity | 100,0%; Fred. No. 5;
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    Homan E 'E pr tela sequence residues 54 531.
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    RICK: h man: EIP like interacting CLARP kinase; apoptosis regulator; ARC;
    tampase to tarpare to: 2006 righalling; up plonis signalling pathway:
Elv
    THE A: THE E. DEEP I: diagnosis: cell growth: apoptosis dysregulation;
    ges therapy, rudgae disorder, cancer; neurodespendrative disorder; AIDS;
EW
    apresti abaemen; ischaemic impary; toxin induced liver disease.
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115
     Homo sapiens.
XX
PN
     W09955134-A2.
X X
     04 - NOV - 1999.
PD
XX
PF
     27-APR-1999; 99WordS09183.
XX
PR
     27 APR 1998; 98US-0069023.
XX
     (UNM) ) UNIV MICHIGAN.
PA
ХX
PΙ
     Numez G. Inohara N. Koseki I;
ХX
DR
     WP1; 2000:072163706.
XX
     Compositions for identitying apoptosis signalling pathway inhibitors
PT
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     useful for treating diseases
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    Claim 6; Page ; 93pp; English.
XX
00
     This sequence is a tragment of the buman RDK (RDD like interacting CLAR)
120
     Finance) protoin of the invention. Fick acts as a positive regulator.
CC
     of apoptosis, potentiating apoptosis induced by cuspase 8 and cuspase 1
     during CD9F signalling. The invention provides methods for identifying
     apoptosis signalling pathway inhibitors and activators, and methods and
120
     compositions for screening compounds which will modulate the interactions
    of the various compositions identified: ARC. RICK, and the CIDE tamily of activators (CIDE A. CIDE B and DREP-1). RICK is useful in screening
cc
cc
     assays for agents, useful in the diagnosis, prognosis or treatment \phit
CC
     disease associated with excess cell growth and dysregulation of
     apoptosis. Complexes containing RICK and CLARP can be used in drug
     screening assays to identify inhibitor molecules blocking CD95-modiated
CC
     apoptosis. Overexpression of ARC in an in vitro cell system can be used
CC
     to identify inhibitors of the enzymatic activity of caspase 8.
CC
     Identification of ARC-like inhibitory compounds may be useful for gene-
73.5
     therapy treatment of disease with increased cell death in muscle fissue
CC
     and cardiac disorders. Therapeutic compositions of CIDEs can be used to
     treat e.g. cancer, AIDS, neurodegenerative disorders, aplastic anaemia,
(10
     ischaemic injury, and toxin induced liver disease. AntiRICK antibodies
     can be used as reasents for the preparation or attinity chromatography
     media, and for diagnostically measuring RICK levels. A specific inhibitor
     of an essential step in the biochemistry of apoptosis is needed. RICK
cc
     interaction with intracellular factors such as CLARP and FADD appears to
1177
     he essential for apoptosis, inhibitors of REME binding to intracellular 🗣
CC
     apoptosis factors are potential drug candidates.
     Note: This seepremee was created using intermation given in the
CC
     specification.
\mathbf{x} \mathbf{X}
     Sequence 478 AA;
SQ
  Cokery Match
                         85.4%; Score 461; DB 21; Length 478;
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  Matches 461; Convergitive 9; Mismatches 9; Indets 9; Gaps
       80 PILGIONEPERIGIVTEYMENGGINELLHEKTEYPDVAW LBURLLHEIALGVNY(HNM) 1 00
Qy
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     Human RICK protein sequence.
ХX
     RICKs bomans RIP-like interacting CIARD bloomer, apopt als regulator, ARC,
YW
     caspase-8; caspase-10; CD95 signalling apoptosis signalling pathway;
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     CIDE-A: CIDE-B: DREP-1: diagnosis; col: growth; apopt six dysteral diagnosis;
     gene therapy; cardiac disorder, cancer, neurodegenerative disorder; AIDS;
۲W
     aplastic shoeds ischedicinjury too meindusel liver discuse
ХX
08
     Homo sapiens.
ХX
    WH9955144 AJ.
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XX
     Numer G. Trochara N. Kogoki T.
PI
XX
     WP1; 2000-072164/06.
DR
DR
     N-PSDR: AAZ48762.
ХX
PT
     Compositions for identifying apoptable signalling pathway inhibitors
PT
     useful for treating diseases
XX
PS
    Claim 1; Fig 7a; 93pp; English.
XX
     This sequence is the human RICK (RIP-1 ke interacting CLARP kinase)
CC
     protein of the invention. The PICK protein acts as a positive regulator
     of apoptosis, potentialing apoptosis induced by caspase 8 and caspase 10
CC
     during CD95 signalling. The invention provides methods for identifying
dd
     apoptosis signalling pathway Inhibitor; and activators, and methods and
00
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00
     compositions for screening compounds which will modulate the interactions
     of the various compositions identified ARC, RICK, and the CIDE family of activators (CIDE-A, CIDE-B and DREP-1) RICK is useful in screening
     assays for adents, useful in the diagnosis, prognesis or treatment of
    disease associated with excess cell quowth and dysregulation of apoptosis. Complexes containing FICK and CLAFF can be used in drag
CC
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     screening assays to identify inhibitor molecules blocking CD95 mediated
     apoptoxis concrexpression of AFC in an is vitra cell system can be used to identify inhibitors of the enzymatic activity of caspase-8.
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     Identification of ARC-like inhibitory compounds may be useful for gene
     therapy treatment of disease with increased cell death in muscle tissue
CC
     and cardiag disorders. Therapeutic compositions of CIDPs cun be used to
     treat e.g. cancer, AIDS, neurodegeneralive disorders, aplastic anaemia,
     ischaemic impary, and to do induced liner discuss. AntibleK untibedies
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can be used as reagents for the preparation or atfinity chromatography
    media, and for diagnostically measuring RECK levels. A specific inhibitor
cc
    of an essential step in the biochemistry of apoptosis is needed. MICK interaction with intracellular factors such as CLAFF and FADD appears to
    be essential for apoptosis, inhibitors of RICK binding to intracellular
CC
    apoptosis factors are petential drug candidates
XX
    Sequence 531 AA:
911
                       85.4%: Score 461; DB 21; Length 531;
 Query Match
 Best Local Similarity 100.0%, Pred. No. 0:
 Matches 461, Conservative 6, Mismatches
                                            0, indels 0; Gaps
      80 PILGIONEPEDES (VIEYMENGOLNE), LHRKTEYPDVAWEEREKI HETALGVNY LHNMT 139
Qy
        Dib
      71 pilgionepetigiyteympagelmollhrkbeypdvawplrftilheialgvvylhumt 130
     14 - PREEBHREEGNILLENHEHVERAFELLEKKEMMSLOGSE BECAPETTILLYMPPENYE 199
         1:1 pp://hhdlkt-p.iildncfhvkiadtglskwrmmslogsissksap.ggtliymppenye 190
Db
     2500 PROCESSAS PRINCIPANAV PREVIOUS REQUESTIVENE QUINTSVAQUESSEVINEES LEYDI 259
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     19) pagkerasikhdivsyavitwovisnkaptodvinpiqimysvsaqbrpvinooslpydi 250
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     21 ) phramibile, asymptomy fik lielop littles these 1914ktklysses 310
     Fig. Althoughthemical indevined Epide (Ostopanions de la reside Alegon) Fasele AQP (379)
         Db
     311 aihlodkkkmolstnipvnhappessaasalhensaspetsislpapadadilsikaad 370
     380 CYFMKUHHUFGNHSWECTIJGSGRAAFTHAKTTFCSSATINFLUTAGNSERLOPGTAQQW 439
         37) cyfmklhhopanhswastis asgraafodhkttpossaii aplstaansei lapqiaggw 430
Db
     440 TQSKREDIVNQMILAGENQSEDALELEDILIMKEDYELVSIKETERISKVRQLEDTTDIQGE 499
         431 lyskredlingsteachepsidallsrdlimkedyelvstkptrtskerglidttdigge 490
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     500 BY ARVIVOR FOREQUEE CONSTRUCTIONS BOARD 540
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        491 - Cak I. gk this highest group of the anapapete tigaken for t
10
RESULT 4
AAY68774
    AAYbo774 standard, frotein, 54% AA.
    AAY68774 +
ΑŒ
ХX
151
    16 MAY 2000 (first entry)
XX
DE
    Amino acid sequence of a homan phosphorylation effector PHSP-6.
    Human, phosphorytation effector, PHSD, proliferative discretize
    immune disorder; neuronal disorder.
KW
ХX
OS
    Homo sapiens
\mathbf{X}\mathbf{X}
                  Location/Qualifiers
1.13
    Kerry
    Region
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                       - "protole kinase family signature requesce"
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    Modified-site
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     and DEC Long
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                      9803 0113796
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     T. AN LOOK
                      9908 0173482
     The JAN Largery
                      9908 0229005
1.14
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     (INCY , INCYL: PHARM INC.
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1.1
     H::Iman G., cal P. Tang Yf, Corley NC, Guegler KJ, Baughn MR;
1-1
     Pitters n.C., Bandman O., Au Young J., Gordone GA., Yue H., Azimzai Y
1 1
     Rolldy F. Lu. AM, Shih LL:
XX
     WE co. 20 183 05716
     N PSDB: AAL46.43
XX
     Now home: phosphorylation effectors useful for the diagnosis, freatment
      and pre-entisk of proliferative, immune and neuronal disorders
XX
123
     Claim I Fage 84 85; 142pp; English.
     AAY 6376 (3%) and AAY68797 39 represent human phosphorylation effectors
     (rime). Resign sted PHSP1 PHSP11 (the protein sequence for PHSP28 is not
     given in the specification). The sequences were isolated from cDNA
     Libraries prepared from various human tissues. The PHSP proteins are
     spectual to the diagnosis, treatment and prevention of proliferative
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disorders, immune disorders and neuronal disorders. The PRSP proteins
CC
       form pharmaceutical compositions which useful for treating or preventing
CC
        disorders associated with decreased PHEP expression/activity. PHSP
CC
        antagonists are useful for treating or preventing disorders associated
cc
        with increased PHSP expression/activity.
ΧХ
SU
        Sequence 540 AA;
                                        85.4%; Score 461; DR 21; Length 540;
   Ouery Match
   Best Local Similarity 100.0%; Pred. No. 0;
   Matches 461; Conservative 0; Mismatches
                                                                            O: Indels O: Caps
           80 FILGDINGFELDGIVTEYMENGGUNELLHKKTEYFDVAWFLKFRILHEIALGVNYLHNML 139
               Db
           80 pilqicnepetlqivt.eympnqsInelThrkt.eypdv.wpTrtritheiaTqvnyThnmt 179
         140 BEFLUHH DETENDED MEHRVEDALFULFERMAMMELEER GEGUEGAFLASSFLYMFFENYE (1996
               140 ppllhhdlkt/pilldmeth/kiadtalskwrmmsls-presksapeggtilymppenye 13 c
Db
         200 POOKSBASTKHO LYSYAVITWEVESEKQPETOVINPLO (MYSVSOSHRPVINEBSLPYD) - 25 +
 ुः
               200 pgqksrasikhdiysyavitwevlsrkqptedvtnplqimysmcqqbrpmineeslpydi 250
125
         260 PREPARMISTIESCWAONPOERPSELECTIELEEVLETEEETELEAVIOLKKIKLOSVSS (19
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          +20 ATHERORERMEDSONTEVNHORGERFSCASSIQUEENCIQUES DESCRIPTION OF TRIBERADO ATTENDADO DE CONTRA CONTRA CONTRA CONTRA CONTRA CONTRA CONTRA CONTRA CONTRA CONTRA CONTRA CONTRA CONTRA CONTRA CONTRA CONTRA CONTRA CONTRA CONTRA CONTRA CONTRA CONTRA CONTRA CONTRA CONTRA CONTRA CONTRA CONTRA CONTRA CONTRA CONTRA CONTRA CONTRA CONTRA CONTRA CONTRA CONTRA CONTRA CONTRA CONTRA CONTRA CONTRA CONTRA CONTRA CONTRA CONTRA CONTRA CONTRA CONTRA CONTRA CONTRA CONTRA CONTRA CONTRA CONTRA CONTRA CONTRA CONTRA CONTRA CONTRA CONTRA CONTRA CONTRA CONTRA CONTRA CONTRA CONTRA CONTRA CONTRA CONTRA CONTRA CONTRA CONTRA CONTRA CONTRA CONTRA CONTRA CONTRA CONTRA CONTRA CONTRA CONTRA CONTRA CONTRA CONTRA CONTRA CONTRA CONTRA CONTRA CONTRA CONTRA CONTRA CONTRA CONTRA CONTRA CONTRA CONTRA CONTRA CONTRA CONTRA CONTRA CONTRA CONTRA CONTRA CONTRA CONTRA CONTRA CONTRA CONTRA CONTRA CONTRA CONTRA CONTRA CONTRA CONTRA CONTRA CONTRA CONTRA CONTRA CONTRA CONTRA CONTRA CONTRA CONTRA CONTRA CONTRA CONTRA CONTRA CONTRA CONTRA CONTRA CONTRA CONTRA CONTRA CONTRA CONTRA CONTRA CONTRA CONTRA CONTRA CONTRA CONTRA CONTRA CONTRA CONTRA CONTRA CONTRA CONTRA CONTRA CONTRA CONTRA CONTRA CONTRA CONTRA CONTRA CONTRA CONTRA CONTRA CONTRA CONTRA CONTRA CONTRA CONTRA CONTRA CONTRA CONTRA CONTRA CONTRA CONTRA CONTRA CONTRA CONTRA CONTRA CONTRA CONTRA CONTRA CONTRA CONTRA CONTRA CONTRA CONTRA CONTRA CONTRA CONTRA CONTRA CONTRA CONTRA CONTRA CONTRA CONTRA CONTRA CONTRA CONTRA CONTRA CONTRA CONTRA CONTRA CONTRA CONTRA CONTRA CONTRA CONTRA CONTRA CONTRA CONTRA CONTRA CONTRA CONTRA CONTRA CONTRA CONTRA CONTRA CONTRA CONTRA CONTRA CONTRA CONTRA CONTRA CONTRA CONTRA CONTRA CONTRA CONTRA CONTRA CONTRA CONTRA CONTRA CONTRA CONTRA CONTRA CONTRA CONTRA CONTRA CONTRA CONTRA CONTRA CONTRA CONTRA CONTRA CONTRA CONTRA CONTRA CONTRA CONTRA CONTRA CONTRA CONTRA CONTRA CONTRA CONTRA CONTRA CONTRA CONTRA CONTRA CONTRA CONTRA CONTRA CONTRA CONTRA CONTRA CONTRA CONTRA CONTRA CONTRA CONTRA CONTRA CONTRA CONTRA CONTRA CONTRA CONTRA CONTRA CONTRA CONTRA CONTRA CONTRA CONTRA CONTRA CONTRA CONT
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               320 aiblindkkkmelinlinipushqipqeerinjsiqlberingiq etisinlipapq findilsikaqd 379
Db
          380 CYEMKLHBOPGNBONDSTEGGGGRAAF DHKETFOSSAFINFESTAGNSERLOPGFAQQW 439
UV
              Ob
          380 cyjimklihhopqoleswist isqsqraatodhkttpcssalinplistagnseriqpqiaqqw 4 ce
         440 TOSKREDIVNOMTEACLNOSLDALLSEDLIMKEDYELVSTKEFERTSKVROLLDITDIQGE 450
UN
               Db
         440 iqskrediocopates (cqs/dailsed) lokedyel etkptrt skyrqlldttdiqqc 455
         500 DEAKVIVSKERDNKSMGLSPYPDILVVSROPSENLLGNKOM 540
07
              500 of akvivaklkinkamalapypoituverepelottankam 540
RESULT 5
AAH43570
       AAB43570 standard; Protein; 544 AA
ID
ХX
AC.
        AAB43570;
XX
DT
       08:FEB 2001 (first entry)
XX
DE
       Human cancer associated protein sequence SEQ ID No:1015
ХX
ΚW
       Human; cancer associated gene; cancer antigen; detection, cancer;
KW
       diagnosis; cytostatic; proliferative; vulnerary; immunomodulator;
       antidiabetic; antiasthmatic; antirheumatic; antiarthritic; antiviral;
KW
        antiinflammatory; antithyroid; antiallergic; antibacterial; cardiant;
KW
        dermatological; nearoprotective; thrombolytic; coagulant; nootropic;
        vasotropic; antipsoriatic; antianglogenic; gene therapy; intlammation
        immune disorder; haematopoietic cell disorder; auteimmune disorder;
KW
KW
        allergic reaction; graft versus host disease; organ rejection;
       haemostatic; thrombolytic; cardiovascular disorder; infection;
KW
ΚW
        neurological disease; drug screening.
ХX
US
        Homo sapiens.
XX
        W0200055350-AL.
i 'N
XX
PD
       21:SEP 2000.
ХX
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08-MAR-2000; 2000W--9505882.
DF
XХ
     12-MAR-1999 - 0909-0194270
PR
XX
     (HUMA:: HUMAN GENOME SCI INC.
PΑ
XX
PT
     Rosen CA, Ruben SM;
XX
     WP3: 2000 507533755
DR
     N ISDB; AAC77779.
DR
ХX
     Novel isolated nucleic acids comprising sequences encoding peptides
PT
PT
     useful for treating or diagnosing e.g. cancer -
ХX
PS
     Claim 11; Page 1595-1597; 2352pp; English.
XX
CC
     AAC77607 to AAC78448 encode the human cancer associated priteins given
     in AAB43399 to AAB44279. The proteins can have activities based or the
CC
CC
     tissues and cells the genes are expressed in. Example of activities
dd
dd
     include: cytostatic; proliferative, vu nerary, immunomodulator,
     antiduabetic: antiasthmatic; antirheum tic; antiarthritic;
     antiinflammatory; antithyrmid; antial orgin, antibacterial, antivical.
CC
     dermatological: neuroprotective; carding; thrombolytic; coagulant; nootropic; vasctropic; antiproriatic and antianglogenic. The
     polynucleotides and polypeptides can be used for preventing, treating or
     ameliorating medical conditions and diagnosing pathological conditions.
CC
     Polynucleotides, polypeptides, antibodies, agonists and antagonists from
     the present invention may be used to treat immune disorders by activating
     or inhibiting the proliferation, differentiation or mobilisation of
     immune cells, to treat disorders of trematopoletic cells, autoimmune
de
     disorders, allergic reactions, graft versus host disease and organ-
     rejection modulate haemostatic or thrombolytic activity, modulate
     inflammation, cancers, cardiovascular disorders, neurological disease and
     bacterial or viral infections. The postides, nucleotides, antibodies,
CC
     agonists and antagonists may be also be used in drug screens. AAC78449 to
     AAC78457 and AAB44240 represent sequences used in the examplification of
CC
     the present invention
XΧ
SQ
     Sequence 544 AA;
  Ouery Match
                         85.4%; Score 461; DB 21; Length 544;
  Best Local Similarity 100.0%; Pred. No. 0:
  Matches 461; Conservative 0; Mismatches
                                                 0; Indels 0; Gaps
QУ
       80 PILC!CHEFEFLGIVIEYMPNGSLNELLHKK!EYPDVAWPLRFR!LHEIALGVNYLHNMT 139
          Db
       84 pilgionepeflgivteymphyslnellhrk/eypdvawplrfrilheialgvnylhhmt 143
      140 POLLHHOLKTONILLDNEFHVKIADFGLSKWUMMSLSQSRSSKSAPEGGTIIYMPFENYE 199
Οÿ
          ÞЬ
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144 pp://hhdlktqcilldnefhrkiadfglskw/mmslsqs/ssksapeggtiiymppcnye 203
     200 FÖÇKERASIKHETIYSYAVITWEVLSRKÖPFEDVINPLÖIMYSVSÇGURPVINEESTETDI 259
QΥ
         2^{64}\ \text{pyrkorus} \\ \text{ikhdiysyavitwevlarkqpfc} \\ \text{dvtnplqimysvsqqlu} \\ \text{pvinceslpydi} \\ \text{ 263} \\
Lib
UΨ
     260 PHEARMISLIESGWAGNEDERPSFLKCLIFFEPVLRTFEEITFLEAVIOLKKIKLOSVSS 319
        <u>្បីក្រុមប្រជាព្រះប្រជាព្</u>ធិបាយមារ៉ាប់បាប់ប្រើបាប់ប្រើប្រែក្រុ
Db
     2:4 phrarmizlicsgwagopdorpeilkelle bepairtfealtiflea.liglkktkligesse 323
     320 ATHLODKKKMELSINIEVNHORDEFESOOSS LHUNSOSPETSESITAEDUNGELSEKAOO 274
QV
        Db.
     321 alblodakko latnipunlap pesagas plenegapetaralpap dedflerkagd 283
QY
     38) CYPMKLHHCPCHHSWDSTISCSQRAAFCD4CTFCCSAIINFLSTAGNSEKLOPGIAQQW 439
        Db
     384 cyfmkihhopanhowistirgsqibafoih.ttp://ssaiingletuqnscriqpqiaqqw 443
     440 FORKALDTANÖMLEVET MÖST EVIT SAMET AKKEDARL ARTRADLAKARÖTT MALDITÖDE. 190-
Qy
        444 igskredivngmteachnysladlerdlimbelyelystkriitskorilldidigge 503
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                  504 of skulu gkikorskoped topopol tonerepsint ignksm 544
RESULT
AAY31140
         AAY31140 standard; frotein; 540 AA.
XX
         AAY3!140:
ХX
         25-00T-1999 (first entry)
XX
         Human CARD=3 protein.
DE
XX
KW
         CARD-3; caspase recruitment domain; CARD-4; regulation; detection;
        case of capture retriction described the strength of the square of the strength of the square capture of the square respective on the square capture of the square capture of the square capture of the square capture of the square capture of the square capture of the square capture of the square capture of the square capture of the square capture of the square capture of the square capture of the square capture of the square capture of the square capture of the square capture of the square capture of the square capture of the square capture of the square capture of the square capture of the square capture of the square capture of the square capture of the square capture of the square capture of the square capture of the square capture of the square capture of the square capture of the square capture of the square capture of the square capture of the square capture of the square capture of the square capture of the square capture of the square capture of the square capture of the square capture of the square capture of the square capture of the square capture of the square capture of the square capture of the square capture of the square capture of the square capture of the square capture of the square capture of the square capture of the square capture of the square capture of the square capture of the square capture of the square capture of the square capture of the square capture of the square capture of the square capture of the square capture of the square capture of the square capture of the square capture of the square capture of the square capture of the square capture of the square capture of the square capture of the square capture of the square capture of the square capture of the square capture of the square capture of the square capture of the square capture of the square capture of the square capture of the square capture of the square capture of the square capture of the square capture of the square capture of the square capture of the square capture of the square capture of the square capture of th
FW
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         hormone dependent tumbur, autoimmune disorder, Alchelmer's discase;
         systemic lupus crythematosis; immune modiated quamorulonephritis; stroke; rurkingon's discase, amyotisphic lateral solerosis; retinitis piamentesa;
KW
EW
K W
         spinal muscular dystrophy; cerebellar degeneration; anaemia; drug;
KW
         myelodysplastic syndrome; myocardial infarct.cn: cell proliferation:
          cell differentiation, cell survival; CARD 41. CARD 43, CARD 47:
KW
         CARD: 42; human.
XX
OS
         Homo sapiens.
ХX
FH
                                       the dation/Qualifiers
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         Domain
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         Doma in
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         Domain
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PN
         W09940102-A1
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         12 AUG-1999.
PD
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                                      99WO-0802544
PF
         05-FEB-1999;
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PR
         08:DEC-1998:
                                      9898-0207359.
PR
         06-FEB-1998:
                                     9805-0019942
         17 JUN:1998,
                                     5883-0099041.
XX
         (MILL ) MILLENNIUM PHARM INC.
PA
XX
PΙ
         Bertin J;
ХX
DR
         Wri, 1999 494269741.
         N-PSDB: AAZU9246
DR
         Novel CARD-3 and CARD-4 genes and polypeptides used or treating
PT
         regulation of cellular proliteration and differentiation and cell
POT
D'I
         survival
ХX
PS
         Example 2: F.q z: 181pp: English.
         This invention describes the isolation of movel human caspase
         re-reliment funding TAFF 3 and CAEF 4 polymonth tides and protoins and a
CC
         partial murine CARD 4L protein and genes. The genes and proteins of
00
          the invention are involved in the requiation of caspase activation.
CC
         The caspase recruitment domain (CARD) polynucleotides, polypeptides,
         homologues and antibodies can be used in acreening assays, detection
         assays, predictive medicine and therapeutic and prophylactic methods of
         treatment. The methods may be used to diagnose and treat patients which
CC
         are suffering from a disorder associated with abnormal level or rate of
         apoptitie well death, aknormal autility of the Fas/APO ? receptor
         complex, absormal activity of the INF incorptor complex, or abiormal
         authority of a aspass or bescassed that may be treated to but come or
         (particularly tellicular lymphoma, carcinomas associated with mutations
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in $53 rd barmone dependent tamours), autoimmune disorders (e.g.
           sy temis augens crythematosis, immune mediated glomerulonephritis), viral
           integrisms, Altheimer's disease, Parkinson's disease, amyotrophic lateral
           scientsis retinitis pigmentosa, spinal muscular dystrophy, cerebeliar
           description, unactual myelodysplastic syndrome, myocardial interction,
           and Proke. PARD 3 protein interacts with other cellular proteins, and so
           can be used for regulation of celliniar proliferation and differentiation.
            and cell carrival. The CAED profess may also be used to for screen drugs
           or compounds which modulate their activity. The CARD 4 gene can express a
           Tona transcript that encodes (ARD 4L, a short transcript that encodes
             "AE 18 or two CAEL 4 spline variants, CAED 4Y and CAED-4X. This sequence
           represents the human CARD's protein described in the method of the
           trive of non-
XX
            Sequence 549 AA:
                                                          566,7%: Score 660; DR 20; Length 540;
    Best Leval Parallarity 99,8% Fred, No. 9;
    Matche: 160: Conservative G. Mismatches
                                                                                                                1, Indels 0; Gaps
                8) FILG: INEPERIGIVERYMENGODNELDHEK STYPDVAWPLEREITHETALGVNYLHNMT 139
                      80 pilai mopotlajistoympiaje sodiški kroypdvi wpliciriško is sapovy Danmi. 139.
146
              140 PPLI HHDLKIQNILLIONEEHVK (ADEGLSKWEMMSLSGSESKSAPEGGI (TYMDDENYE 199
                      ana dan manuspersionem distribution dan alla
Di.
              14. pp.H.hmdlktqn:H.dnethoki.ndtqlskwrmmslsqsrssks.poopqtiiymppenye. 199
UF7
              200 PODKSPASIKHDIYSYAVIIWEVLSRKQPFEDVINPLQIMYSVSQGHRPVINEESLPYDI 259
                          - 181 - 22 - 181 - 18 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 181 - 1
               300 parjkan erakt dayayani twontankig to hitajil jir yanniqila puince sili ydi. 259
1.4
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              260 PHEARMISLIESCWAONEDERPSELECTIELECVLETFEETTELEAVIOLEKTELOSVSS 319
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           common dalata; antiintlammatery; apoptosis; diagnosis;
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       Domain
                                  Zhote "CARD"
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       WO200100826:A2
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        28 JUN 2000; 2000WO 0817691
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        28 JUN 1999: 9908 0340620.
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        (MILL ) MILLENNIUM PHARM INC
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        Bertin J:
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       WPI; 2001 061974/07.
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       N-PSDB; AAF30001.
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        Isolated intracellular proteins predicted to be involved in regulating
        disease activation are used for diagnosis and treatment of e.g. cancer,
PT
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        viral intections, autoimmune diseases, neurological diseases and
        haematological disorders -
11
ХX
       Claim 9; Fig 2; 208pp; Figlish.
DC
ΧХ
        The present sequence is that of human caspase recruitment domain s
CC
CC
        (CARD-3), an intracellular protein predicted to be involved in
        regulating raypage actimation. The sequence is predicted from an
CC
        isolated CDNA clone (see AAF30001). Methods of diagnosing and
CC
        treating patients suffering from a disorder associated with an
CC.
       abnormal level or rate of apoptotic cell death, abnormal activity
       of the PasyAPO I receptor complex, abnormal activity of the tumour
       necrosis factor receptor complex or abnormal activity of a caspase
       involve administering a compound that modulates the expression or
CC
       activity of CARD-4, CARD-4, CARD-5 or CARD-6 e.g. using gene
       therapy methods. Such disorders include cancer, viral intection,
(1)
CC
       autoimmune disorders, neurological diseases, haematological
620
       disorders, inflammatory disorders and immune disorders. CARD 4.
        4, 5 and 6 proteins can be used to regulate cell proliferation.
       cell survival and cell growth. They can also be used to screen
CC
       drags or compounds that modulate their activity or expression and
        to freat disorders associated with insufficient or excessive
de
       production of CARDER, 14, 15 or 16 protein, or production of an
170
       aberrant protein.
ΧX
       Sequence 540 AA
   Query Match
                                         66.7%; Score 460; DB 22; Length 540;
   Best Local Similarity 99.8%; Pred. No. 0;
   Matches 460; Conservative 0; Mismatches 1: Indels 0; Gaps
           80 FILGIONEPERIGIVTEYMENGSINELIHKKTEYEDVAWELKEFILHENALGVNYLHNMI 159
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               Dib
           80 pilgicnepetlgivteympngslmellhrkteypdvawplrtrilheialgvnylhnmt 139
          140 PPLAHHOLEIGNIGINEERVEIADEGLSEWEMMSLSGSESSESAPEGGTIIYMPPENYE 199
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       380 CYFMKLHHCPGNHSWDSTISGSQRAAFCDHKTTPC;SAIINPLSTAGNSERLQPGIAQQW 439
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           380 cyfmklhhcpgnhswdstisgsqraafcdhktipc;saiinplstagnserlqpgiaqqw 439
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       440 IQSKREDIVNQMTEACLNQSLDALLSRDLIMKEDYELVSTKPTRTSKVRQLLDTTDIQGE 499
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       500 PPAKVIVOKIKDNKOMGLOPYPELLVVSRSPSENI ONKSM 540
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RESULT
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AAY59406
      AAY59406 standard: Protein: 284 AA.
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      AAY59406;
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      21-MAR-2000 (first ontry)
DT
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      Human kICK protein sequence residues 248-531.
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ХX
      RICK: Figure Fig-11ke interacting CLAFF kinases apoptosis regulator: ARC:
ΚW
      caspase-8; caspase-10; CD95 signailing, apoptosis signailing pathway, close-8; Close-8, DPEP-1; diagnosis; cell growth; apoptosis dysregulation;
KW
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      gene therapy; cardiac disorder; cancer; neurodegenerative disorder; AIDS;
ΚW
      aplastic anaemia ischaemic intury; tox.n-induced liver disease
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DS
      Homo sapiens.
 ХX
PN
      W09955134-A2
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      04 - NOV - 1999
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 PF
      27-APR-1999.
                        99WO-US09183
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      27-APR-1998;
                        9808-0069023.
       (UNM1 ) UNIV MICHIGAN.
 XX
       Nunez C. Inohara N. Koseki T;
 PΙ
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      WPI: 2000-072163/06.
 DR
 ХX
       Compositions for identifying apoptosis signalling pathway inhibitors
       useful for treating diseases
       Claim 6: Page -: 93pp; English.
 XX
       This sequence is a fragment of the human RICK (RIP-like interacting CLARP
 CC
CC
       kinase) protein of the invention. RICK sets as a positive regulator
       of apoptosis, potentiating apoptosis is luced by cuspase 8 and cuspase-10
 čč
       during CD95 signalling. The invention provides methods for identifying
       apoptosis signalling pathway inhibitors and activators, and methods and
      compositions for screening compounds which will modulate the interactions of the various compositions identified: ARC, RICK, and the CIDE family of activators (CIDE A, CIDE-B and DREP-1). RICK is useful in screening
       assays for agents, useful in the diagnosis, prognosis or treatment of
       disease associated with excess cell growth and dysregulation of apoptosis. Complexes containing RICK and CLARP can be used in drug
       apoptosis. Complexes containing RICK and CLARF con to use in Group servering assays to identify inhibitor molecules blocking CDDS-mediated apoptosis. Overexpression of ARC in an in vitro cell system can be used to identify inhibitors of the enzymatic activity of caspase-R Identification of ARC-like inhibitory compounds may be useful for gene therapy treatment of discase with increased cell death in muscle tissue
       and cardiac disorders. Therapeutic compositions of CIDEs can be used to
       treat e.g. cancer, AIDS, neurodegenerative disorders, aplastic anaemia,
       ischaemic injury, and texin-induced liver disease. AntiRICK antibodies
       can be used as reagents for the preparation or affinity chromatography
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media, and for diagnostically measuring RICK levels. A specific inhibitor
          of an essential step in the biochemistry of apoptosis a specific inhibitor of an essential step in the biochemistry of apoptosis is needed. RICK interaction with intracellular factors such as CLARP and FADD appears to be essential for apoptosis, inhibitors of RICK binding to intracellular
CC
CC
           apoptosis factors are potential drug candidates.
 CC
           Note: This sequence was created using information given in the
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dd
           specification.
 XX
           Sequence 284 AA:
 SQ
     Query Match 52.6%: Score 284: DB 21; Length 284: Best Local Similarity 100.0%, Fred. No. 1.3e-283; Matches 284: Conservative 0: Mismatches 0: Indels
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            AAM93621 standard; Protein; 540 AA.
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             AAM93621:
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             06-NoV-2001 (first entry)
  DOM
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             Human polypeptide, SEQ ID NO: 3454.
  DE
  XX
             Human; full length cDNA, cDNA synthesis; oligo-capping.
   ХX
            Homo sapiens.
   ХX
             EP1130094-A2.
   PN
   ХX
             05-SEP-2001
   PD
   XX
             07-Jun.-2000; 2000EP-0114089.
   ХX
             08-JUL-1999; 99JP-0194486.
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             ota I. Nishikowo T. Inodoi T. Havashi K. tehli S. Kawai Y.
Wakamatsu A. Suqiyama T. Naqai K. Kojima S. Jisuki I. Koqa H.
   FI
              WPT: 2001-524255/58
   DR
              N-PSDB; AAK94554.
   DR
              830 Primers useful for synthesizing full length cDNA clones and their
   DT
              use in genetic manipulation
   PT
    ХX
              Claim 8; SEQ ID NO 3454; 1380pp + sequence listing; English.
    PS
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The it entire relates to primers for synthesising full length cDNA.
           closes 830 cDNA molecules encoding a human protein have been
           applied and sucleotide sequences of 5% and 3% ends of the CDNA
           acceptures have been determined. Primers for synthesising the full length
            SDNA are useful for clarifying the function of the protein encoded by
           the CLWA The full length clones were obtained by construction of full
           sength carry and cDNA libraries that were synthesised by the oligo capping
           method. The primers enable the production of the full length cDNA easily
          without my special methods, the present sequence is a polypoptide
           schooled by a full length human conA of the invention.
           Note: he sequence data for this patent did not form part of the printed
            specification, but was obtained in the ROM format directly from EPO.
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             equence 51 AA.
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                                                      - 48.0%; Schare 259; DB 22; Length 540;
    Best Local Similarity (99.6%) Fred. No. 1.3e 257;
    Matches log Conservations to Mismatches
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                     140 ppillhhd.ktqnilldnethykiadfqlakwrmmslagsrssksapeqqtiiymppenye 199
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          Hamas E 'K pr term sequence residues 365 531.
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           FOCK: homan: FIP like interacting CLARP kinase; apoptosis regulator; ARC;
           trapase to calpase 10: Clob signalling, apoptosis signalling pathway;
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          COOK A: CIDE B: DREP 1: diagnosis; cell growth; apoptosis dysregulation;
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          generative disorder: concer; neurodegenerative disorder; AIDS;
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           ap.astr = maggra, ischaemic impary; toxim induced liver disease.
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    27 APR-1998; 98US 0069023.
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    (UNMI ) UNIV MICHIGAN.
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    Numez G, Inohara N. Koseki T;
ΧХ
    WPI: 2000 072163706.
DR
XX
    Compositions for identifying apoptosis signalling pathway inhibitors
PT
P1
    useful for treating diseases
ХХ
PS
    Claim 6; Page ; 93pp; English.
XX
    This sequence is a tragment of the human RICK (FIP-like interacting CLARP
CC
120
     kinase) protein of the invention. RICK acts as a positive regulator
    of apoptosis, potentiating apoptosis induced by caspase 8 and caspase 15
00
    during CD95 signalling. The invention provides methods for identifying
CC
    apoptosis signalling pathway inhibitors and activators, and methods and
    compositions for screening compounds which will modulate the interactions
    of the various compositions identified: ARC, RICK, and the CIDE family of activators (CIDE-A, CIDE-B and CREE-1). RICK is useful in screening
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    assays for agents, aseful in the diagnosis, prognosis or treatment of
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    disease associated with excess cell growth and dysregulation of
CC
    apoptosis. Complexes containing RICK and CLARP can be used in drug
    screening assays to identify inhibitor molecules blocking CD95 mediated
ere.
    apoptosis, overexpression of ARC in an in vitro cell system can be used
120
     to identify inhibitors of the enzymatic activity of caspase 8.
    Identification of ARC-like inhibitory compounds may be useful for gene
(*(*
    therapy treatment of disease with increased cell death in muscle tissue
    and cardiac disorders. Therapeutic compositions of CIDEs can be used to
    treat e.g. cancer, AIDS, neurodegenerative disorders, aplastic anaemia,
(2/2
    ischaemic injury, and toxin-induced liver disease. And aRICK antibodies
     can be used as reaports for the proparation or affinity chromatography
(27)
    media, and for diagnostically measuring RICK levels. A specific inhibitor
    of an essential step in the biochemistry of apoptosis is needed. RICK
CC
    interaction with intracellular factors such as CLARP and FADD appears to
    the essential for apoptosis, inhibitors of RECK binding to intracellular
    apoptosis factors are potential drug candidates.
     Note: This pegagage was greated using information given in the
CC
    specification.
XX
    sequence 167 AA;
                         30.9%; Score 167; DB 21; Length 167;
 Query Match
 Best Local Similarity 100.0%, Prod. No. 2.3e 163;
 Matches 167: Conservative 0: Mismatches 0: Indels 0: daps
      37.4 Therall typemether in indical fit is algebraic upen to all normal influctations a_{ij} (4) + 3
         1 sikaqdoytiik!hhopanhswdstisasqiaatedhkttpcssaiinplstaanserlqp 60
Oto
     434 GIAQQWIQSKPEDIVNQMTEACLNQSIDALLSPDLIMKEDYELVSTKPTRTSKVRQLLDL 493
Oy
         Db
      61 qiaqqwiqskrodiynqmtoaclnqsldallsrdlimkodyoirstkptrtskvrqlldt 124
UV
     494 IDIQGEEFAKVIVQKI.KUNKQMCLQFYPETI.VVSRSESENLLQNKSM 540
        121 tdliggeofakvivgk!kdnkgmglgpypei(vvsnsps):!/pp.ksm 167
RESULT 11
AAB58938
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HD
XX
    AAR58938:
AC.
ХX
    27 MAR 2001 (first entry)
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```
Breast and ovarian cancer associated antigen protein sequence SEQ 1D 646.
     Human; breast cancer, ovarian cancer, cylostatic; immunosuppressive;
     nonlinear catery over an extensive to detail a minimum suppressive; nootropic; neurpprotective; antiviral, antiallergic, hepatotropic; antidiabetic, antiinflammatory, antivice; vulnerary, anticonvulsant, antibacterial; antifundal; antiparasitic cardiant; immune disorder;
KW
EW
ΚW
     Addison's disease, allergy, autoimmune bremelytic anaemia;
ΚW
     autoimmune thyroiditis; diabetes melliti; Crohn's disease;
KW
KW
     multiple selectsis; rheumatoid arthritis ulcerative colitis,
KW
     cardiovascular disorder; wound healing; neurological disease.
ХX
OS
     Homo sapiens.
XX
     WO200055173-41
PN
XX
     21-SEP 2000.
χ.у.
     08-MAP-2000: 2000W0-US05881
ХX
PR
     12-MAR-1999; 99US-0121270.
XX
     (HUMA=) HUMAN GENOME SCI INC.
PA
XX
     Rosen CA. Ruben SM;
D T
XX
     WPT: 2000-611515758
DR
DR
     N-PSDB; AAF21841.
XX
PT
     New human breast and ovarian cancer associated gene sequences and the
PT
     polypeptides encoded by these genes, useful in the prevention,
PT
     treatment and diagnosis of cancer, immuse disorders, cardiovascular
PT
     disorders and neurological diseases -
XX
PS
     Claim 11; Page 1086; 1299pp; English.
XX
     Sequences AAF21614 \pm AAF22031 represent DNA sequences encoding human
CC
     proteins AABE9711 · AABE9129. The DNA and protein sequences are
CC
     associated with breast and ovarian cancer. Included in the invention are sequences AAP22032 - AAP22040 and AAB59109 which are used in the
CC
CC
CC
     isolation and characterisation of the DNA and protein sequences of the
CC
     invention. The breast and ovarian cancer associated DNA, protein, agonist
CC
     or antagonist sequences exhibit cytostatic; immunosuppressive;
ČĆ
     mostreple, neuroprotective, antiviral, astiallergic, hepatotròpic,
CC
     antidiabetic, antiinflammatory, antiulous, yulnegary, anticonvulsant,
CC
     antibacterial; antifungal; antiparasitic and cardiant activity. The
CC
     polynucleotide and profein sequences are used in the diagnosis of cancer,
CC
     particularly breast and ovarian cancer. The nucleic acid sequences,
     proteins, aged ists and agenists may also be used in the diagnosis,
CC
     prevention and treatment of immune disoriers e.g. Addison's disease,
     allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis,
CC
     diabetes mellitus, Crohn's disease, multiple sclerosis, rhoumatold
     arthritis and ulcerative colitis; cardiovascular disorders such as
     mycoardial isobaemias; wound healing; neurological diseases such as
CC
     cerebral anoxia and epilopsy; and infectious diseases
XX
     Sequence 153 AA.
SO
  Ouery Match 23.3%; Score 126, DE 21, Length 153, Best Local Similarity 100.0%; Pred. No. 3.4e-121; Matches 126, Conservative 2, Mismatches 3, Indels
       97 YMENGSI NELI HEKTEYEDVAWEI PER LIHETAL SZNYLHNMTERLI BHELKTONILLEN (156
           1 ympngslaelihrkteypdvawplrfrilheialg.nylhnmtppllhhdlktqnillda 60
Db
       157 EFEVETADECLSKWEMMSLSGSRSSKSALBOCHT:/MELENYBHDQKSRAStKHLTYSYA DIG
Ov
           61 - Parkia Highskwinnesh sysraaksa pegatii, ma penyepegkaraa ikhdiyaya 120
Db
       217 VITWEV 222
ÜΫ
           11111
Db
       121 vitwer 126
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RESULT 12
AAM25501
     AAM25501 Standard, Protein, 142 AA.
ED
XX
AC.
     AAM25501:
DT
     16 OCT 2001 (first entry)
DE
     Human protein sequence SEQ ID No:1016.
XX
     Human; cancer; ulcer; HIV infection; human immunodeficiency virus;
KW
     antiinflammatory; antirhoumatic; antiarthritic; immunosuppressive;
     antibacterial; endocrine; cardiant; contral nervous system; virucide;
     anti-HiV, fungicido, antimutages, cardicvascular; actianaemic; acaemia;
     antiaggregant; haemostatic; vulnerary; activicer; estecpathic; eczema: dermatelegical; antiallergie; antiasthmatic; actidiabetic; cytestatic;
r.w
     neuroprotective; antidepressant; neotropic; antiparkinsonian; infection;
     immunestimulant, gene therapy, antisense therapy, vaccine; inflammation:
     antianaphylactic; rheumatoid arthritis; septic shock; pancreatitis;
     cardiac dysfunction: neuropathology; cardiac acaphylaxis; autoimmunity
     genetic disease; haematopoietic disorder; platelet disorder; asthma;
     thrombocytopacnia, ostcoporosis, severe combined immunodeficiency:
KW
     allergic rhinitis; diabetes: multiple sclerosis; depression:
EW
     Allholmer's discuse, Parkinson's discase, your degenerative disorder:
     neurological disorder.
ХX
     Homo sapiens
ХX
     WO200153455 A2.
1211
XX
     26-JUL-2001.
PD
XX
\Gamma'\Gamma
     22 DEG 2000; 2000WG US35017.
ХX
      20 pm: 1999, 9900 0471275.
PE
     21-JAN-2000; 2000US-0488725.
25-APE 2000; 2000US-0552317.
T- Fe
PP
хx
i ·A
     (HYSE ) HYSEQ INC.
XX
     Tang Yi, Liu C, Fermanac RT;
PI
XX
DR
     WPI; 2001-457603/49.
     N.PSDB; AAH99442.
XX
      isolated human pulph wheatides encoding polypoptides, aschol for the
      treatment and diagnosis of e.g. caucer, wicers and HIV infection -
PT
ХX
     Claim 20; Page 209; 1217pp; English.
PS
ХX
     AAH99166 to AAH99904 choose the human proteins given in AAM25925 to
     AAM25962. The proteins can have activities based on the tissues and
     cells they are expressed in, such as: antiinflammatory; antirheumatic;
cc
CC
     antiarthritic; immunosuppressive, antibacterial, endocrine; cardiant;
     central nervous system; virucide; anti HIV; funcicide; antimutagen;
CC
     cardiovascular; antianaemic; antiaggregant; haemostatic; vulnerary;
      antiuleer, osteopathic, dermatological, antiallergic, antiasthmatic;
     antidiabetic: cytostatic: neuroprotective: antidepressant: nootropic;
     untiparkingonium, und immunostibulunt. The proteins and polynucleotides
     encoding them can be used in gene therapy, antiscuse therapy and vaccine projection. The proteins and polymerlectides are useful for screening tor
CC
خرد
     agonists or antagonists of a protein and for the treatment and diagnosis
     of disorders associated with the activity of a protein e.g. inflammation,
     rheumatoid arthritis, septic shock, pancreatitis, cardiac dysfunction, seur-pathology, cardiac anaphylaxis, viral, bacterial, HIV and fungal infections, autoimmunity, genetic diseases, bacmatopoletic disorders,
CC
CC
      unaemia, platelet disorders, thromboeytepaemia, wounds, burno, ulcers,
     osteoporosis, severe combined immunodeficiency, eczema, allergic rhinitis, asthma, diabetes, cancer, multiple silerosis, depression,
CC
20
     Alpheimer's discuse, Parkinson's disease, scurodegenerative and
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neurological disorders.

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Be prender 14. AA;
  guerry Matters
                           -i.9%; Score 10; DB 22; Length 142;
  Best Local Similarity 100.0%; Fred. No. 6,036,
  Matches . As Conservative 0: Mismatches 0: Indels 0: Caps 0:
      Tibe DistigNILLIO 155.
          11 1.111
       54 distensifiance
FERTULA 13
AAUL/23
10 AAUL/23 Stanford; Protein: 167 AA.
XX
     AAU1727 :
\mathbf{Y} \cdot \mathbf{Y}
    .o/ N⊝V .ebl (tirst entry)
XX
     Novel signal transduction pathway protein, Seq ID 800.
    Neuroprofestive, cytostatic, dermatological, immunosuppressive, tumour,
     antiinf (ammatory) anti HIV; antibacterial; antiinflammatory; cancer;
     immune system disorder; rheumatoid arthritis; inflammatory condition;
     organ transplant rejection; infection; hepatitis C; blood disorder;
     sickle > 11 anaemia; hyperprofit rative disorder; daucher's discase;
     neurodesemerative discret; Algeiser's disease; Parkinson's disease;
     Stromonomai almormality, Bown Syndroma, Eschaemia, renal dizorder,
     cardiovaccular: respiratory; we med healing; endocrine; Addison's discuse;
     reproductive system; quastrointestinal; liver disorder; AIDS;
     ampaired ammona deficiency syndrome.
XX
     Hower Saymons.
    William A.
. N
1111
     or, AUG . Foll
XX
     I' TAN LUMBER CHOING USOLUZ.
     34 JAN 2000; 1000UR 0179065.
     04 FEB : 000; :0000US 0180628
1.10
     24 FEB 2000; 1000HS 0184664
     02 MAR 2 000; 2000000 0186350
     16 MAR . 000; .000US 01898/4.
     I/ MAR / 000; . 000000 0190076.
    Th APR 2000; 2000US 0198123.
    THE MAY 1900; 100008 0205515
     92 HIN 900; 300HS 0209467;
     .28 JUN .090; 200008 0214886.
     30 JUN 2000; 2000US 0215135;
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    -07 JUL 2000; 2000US 0216880.
     14 JUL 2000; 2000US 0217487.
    -11 JUL 2000; 2000US 0217496;
     11 JUL 5000; 2000US 0218290.
    -25 JHL 900; 2000B 0220963.
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     14 AUG 2000; 2000US 0235266;
    -11 AGG -000; .000US-0225267.
    -14 AUG . 0000; I chord ellister.
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    -11 AUG . 000; 1000US 0225757
     11 AUG : 0000 : 0000FS 0225758;
118
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PR 22 AUG 2000; 2000US:0226681 22-AUC-2000: 2000US:0226868. PR 22 AUG 2000; 2000UC 0227182. 23-AUG-2000; 2000US-0227009. 30-AUG 2000; 2000US-0228924 -01 SEP 2000; 2000US 0229287 01-SEP-2000: 2000US-0229343. 01-SEP-2000; 2000US 0229344 01-SEP-2000; 2000US 0229345 05-SEP-2000; 2000US 0229509 -05-SEP-2000; 2000US-0229513 -06-SEP-2000; 2000US 0230437 -06-SEP-2000; 2000US-0230438 08-SEP-2000; 2000US-0231242. -08-SEP-2000; 2000US 0231243. 08 SEP 2000; 2000US-0231244. -08-SEP-2000; 2000US-0231413. 08-SEP-2000; 2000US-0231414. 98-SEP-2000; 2000US-0232080. -08-SEP-2000; 2000US 0232081. 12-SEP-2000; 2000US 0231968. -14-SEP-2000; 2000US-0232397. 14-SEP-2000; 2000US-0232398. PE 14 CEP 2000; 200005-0232399. 14-SEP-2000: 2000US:0232400. PP PR 14-SEP-2000; 2000US-0232401. PR 14-SEP-2000; 20000S-0233063. PE -14 SEP 2000; 2000US 0233064. 14-GPP-2000: 2000US-0233065. FR 21 SEF 2000; 2000US 0234223. 21-SEP-2000; 2000US-0234274 25-SEP-2000; 2000US-0234997 25 SEP 2000; 2000US-0234998 26-SEP-2000; 2000US-0235484. 27-SEP-2000; 2000US-0235834 27-SEP-2000; 2000US-0235836. 29 SEP 2000; 2000US 0236327 29-SEP-2000; 2000US 0236367 29 SEP 2000; 2000US 0236368. 29-SEP-2000; 2000US 0236369. 29-SEP-2000; 200008-0236370. -02 OCT 2000; 200000 0236802 -02-OCT-2000; 2000US 0237037 -02-OCT-2000; 2000US:0237038. 02-001-2000; 2000US-0237039. 92-OCT-2000; 2000US-9237040. 14-OCT-2000; 2000US-0239935. 13-OCT 2000; 2000US-0239937 20-OCT-2000; 2000US-0240960. 20-OCT-2000; 2000US 0241221 20-OCT 2000: 2000US-0241785. 20-OCT-2000; 2000US-0241786. 20-OCT 2000; 2000US-0241787. 20 -OCT - 2000; 2000US - 9241808 20-OCT-2000; 2000US-0241809. 20-OCT-2000; 2000US:0241826. 01:NOV-2000; 2000US-0244617 08-NOV-2000; 2000US 0246474 08-NOV 2000; 2000US-0246475. 08-NOV-2000; 2000US-0246476. -98-NOV-2000; 2000US:0246477 -08-NOV-2000; 2000US-0246478. -08-NOV-2000; 2000US-0246523. 08-NOV-2000: 2000US-0246524. 08-NOV-2000; 2000US 0246525. 08 NOV-2000; 2000US-0246526. 08 MOV 2000; 2000US 0246527. 08-NOV-2000; 2000US-0246528 08 NOV 2000; 200000 0246532. -08-NOV 2000; 200000 0246609 08-NOV-2000: 2000US 0246610. -08 NOV-2000; 2000US-0246611. -08-NOV-2000; 2000US 0246613.

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17-NOV-2000; 2000US-0249207.
      17 NoV 2000; 2000US 0249208.
      17-NoV-2000; 2000US 0249209.
      17-NOV-2000; 2000US-0249210.
      17-NOV 2000: 2000US-0249211.
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17-NOV-2000; 2000US-0249297
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      05-DEC-2000; 2000US 0251030
PR
      05-DEC-2000; COOMES 0251088
      02-PEG-3000- 3000HB-03E6210
      06-DEC-2000; 2000US 0251479.
      08-DEC-2000; 2000US-0251856.
      08-DEC 2000; 20000S-0251868.
      08-DEC-2000; 200008-0251869.
      08-DEC-2000: 2000US-0251989.
      08-DEC-2000; 200008-0251990.
      11-DEC-2000; 2000US 0254097
      05-JAN-2001; 2001US-0259678.
"XX
      (HUMA:) HUMAN GENOME SCI INC.
PA
ХX
PI
      Rosen CA, Barash SC, Ruben SM;
ХX
DR
      WPI: 2001-165460/50.
DR
      N-PSDR; AAS27152.
ХX
PT
      Novel polypeptides useful for diagnosing, treating, preventing and/or
PT
      prognosing disorders related to the proteins, including cancers, immune
DT
      disorders and neuronal disorders
XX
     Claim 1: SEQ ID No 800; 880pp; English
PS
XX
ad
ad
      The invention relates to novel isolated polypertides (!), and
      polynucleotides (II). (I), (II) and the antibody to (I) are useful for
CC
      diagnosing, presenting and treating diseases including immune system.
CC
      disorders (e.g. congenital and acquired immunodeficiencies, autoimmune
      disorders (e.g rheumatoid arthritis), inflammatory conditions, organ-
      transplant rejections and graft versus host disease, infectious diseases (e.g. hepatitis C), bleeding disorder: haemoglobin abnormalities and
-cc
      other blood-related disorders (sickle cell anacmia), mycloproliferative
      disorders, primary become topoletic disorders, hyperprolliferative
ge
ee
     disorders (e.g. Gaucher's disease and cancer), herrodequeerative disorders (e.g. Alzheimer's disease, barkinson's disease), chromosuma!
      abnormalities (Down syndrome), ischagaig injury (e.g. stroke), renal-
CC
      disorders (e.g. glomerulonephritis), andiovascular disorders
CC
      (e.g. arrnythmia), respiratory disorders, dermatological disorders, in
      wound healing, epithelial cell prolifyration, endocrine disorders (e.g.
      Addition's disease), reproductive syst modisorders, quatrointestinal
CC.
     disorder (inflammatory disorders), liver disorders (cirrhosis),
      as stimulators of B cell responsiveness to pathogens, activators of
CC
      1-ceils, to induce higher affinity artibodies, and as a means to induce
     tumour proliferation in pathologies (.q. acquired immune deficiency systemae (ADES) AANITOSE-AANITESE represent newel signal transletic. pathway protein amino acid sequence of the invention.
                              1.9%; Score 10; DB 22; Length 167;
  Best Local Similarity 100.0%; Pred. to. 0.1;
  Matches 10: Conservative 0: Mismatches 0: Indels 0: Gaps 0.
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146 GURTONILLD 155
           111111111
Db
         4 diktanilld is
RESULT 14
AAU17241
110
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     AAU17241;
XX
     07 NOV 2001 (first entry)
     Novel signal transduction pathway protein, Seq 10 806.
     Neuropriteitle, sytostati, dermatological, hamanosuppressiver tumour:
     antiluflammatory; anti-HIV; antibacterial; antiintlammatory; cancer;
     immune system disorder, rheumatorid arthritis, inflammatory condition; organ transplant rejection, intection, hepatitis c. blood disorder;
     sickle cell anaemia; hyperproliferative disorder; Gaucher's disease;
     mearodetenerable disorder. Alcheimer's disease, larkinson's disease;
     thromosemul abnormality, E.wn., yndrome, ischaemia, renul disorder; candicussedar, respiratory, whand bealing, endemine, Addison's disease:
     reproductive system, quastreintestinal, liver disorder; AIDS;
KW
     acquired immune deficiency syndrome.
ΚW
ХX
     Homo sapiens.
OS
ХX
L1 NJ
    W0200154713 AL
XХ
PD
     02 AUG 2001
XX
E.1.
     17 JAN 2001, 2001W00-US01412.
XX
PR
     31-JAN-2000; 200098-0179065.
PR
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PR
     24 : PEB-2000; 2000US: 0184664.
     02 MAR 2000; 200008 0186350.
     16 MAR-2000; 2,000HS-0189874.
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     18-APR-2000; 2000US-0198123.
     T9 MAY-2000; 2000US-0205515.
     07 JUN-2000; 2000US-0209467
     28 JUN 2000; Decens 0214886
     30 JUN-2000; 2000US-0215135.
     02 JUL 2000; 2000US-0216647.
     07 JUL-2000; 2000US-0216880
     11 Jul. 2000; 2000US 0217487.
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     26 JUL 2000, 200008 0220963.
     26-JUL-2000; 20 JUS-0220964
     11 AUG 2000; 2:- E 0224518
14 AUG 2000: 2 DEUE 0224519
nρ
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     14 AUS 2000, 2000H8 0225214
THE
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PK
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1:37
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22 ARG 2000; 230005:0226581
22 ARG-2000; 200005:0226868
     22\ \text{AMG}\ 2000;\ 20000S\ 0227182
D.D.
DR
     23 AUG:2000: 2000US-0227009
1 R
     30 AUG-2000; 2000US-0228924
DR
     01-SEP-2000; 2000US-0229287
PR
     01 SEP 2000, 20000S 0229343
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101 John 2006 CHOOLES 0229 644
     of strictions, goodfs againsts
     2004 P. 2000 F. 200008 02:29509
     95 (C) 100 (2000) 20000013 (C)200513
     106-SUP 2001: 20000BS 0230437
     106 Sec. 2006-1 2000018 0230438
     of a state 2000 . For another 0.74\,24\,2
     004 (0) 1 (200 ) 200 (0) 8 (02 (124 ) 004 (8) 12 (1244) 200 (0) 18 (02 (1244)
128
     OFF SEC 2000: 2000US 0231413
      78 Sec. 2006. 2000US 0231414
13
      OR $8 F 2000 2000UB 0232000
      not $800 poor __porotts ogspools
      12 SEP 2000, 2000HS 0231968
      14 Str. 2005; 2000HS 0232397
      14 SEC 2000 2000HS 0232 C98
     14 SEC 2000 2000018 02 (23 99
      44 SEE 2006 20000BS 0232400
      14 SEC 2006, 2000US 0232401
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      14 Ste 2004 2000HS 02 G06 C
      14 (St) 2000 2000HS 0233064
      14 SEC 2000 2000018 02 COGS
     21 St. 2006, 2000US 0234223
     .1 SE: .000 2000HS 0234274
     25 St 2000 2000HS 0234997
1.37
     The SECTION COMMISSION OF GRAPHS
     26 SE 2000, 2000HS 0235484
     1. SE 2000 2000US 0235834
     1.7 SEC 1000 2500003 02 CH G
     29 SEC 2000 20000B 0236327
     29 SEc 2000 2000HS 03 05 67
     29 SE 2010), 2000HS 0236 668
     1.9 SE 2000) 2000HS 0236-039
      19 SEC 2000 20000B 02 03 Oct.
     Sep (00), 2000, 20000B 0236802
      SE OCT 1900, 2000UB 0237037
      spinor, postuling midge mixtores,
      52 OC 2300: 2000 BS 6237039.
     92 oct 2000, 2000HS 0237040
     (4.4. oc), 20000, 20000BS 0233935.
      1.3 OC 1.000; 2000HS 0239937
     (2000\,\mathrm{erg}^2) , restrict the mostly of 24.300\,\mathrm{erg}
     2000 2000 2000 BOOMS 0241221
     277 OC. 2000; 2000018 0241785
     2 00% 2000 2000018 0241786
2 00% 2000018 0241787
     The order from South 024 (808
     да окт. долог, долоных од41мом.
     1.0 mil . ot; 2000018 0241876
       1 NOV 2 981; 200900B 0244617
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     FOR NOV 2000; 2000HS 02454 4
     THE NOV 2000; 2000018 0246475
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     FOR NOV 2 670; 2000/08 0246477
     THE NOV 2000; 2000HS 0246478
     or NOV 2000; 2000US 0246523
     FR NOV 20000, 2000005 0246524
     18 NOV 16 00, 20000$ 0246525
     \sim 8~\text{NeV} , thus involude 0.2465.26
1.14
     THE NOV THEMS 2000HS 0246527
      or NoV 2000; June 18 0246528
     THE NOVEL OF STREET NORTHS (024) 05 (2)
      P. NOV. 12 000, 2000/08 0246609
     THE NOVELOUGH PROPERTY OF A GET IN
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1 15
      OB NOV LOSU: 2000US 0246611
     \cos(3\omega V) . Fig. calculus 0.246613
     4.1 NoV . - - - - - . 30048 0249207
     T'NOV TO BE PROPER STRAIGHT
     17 NoV .000; 2000HS 0249209
     10 NoV 10000 100008 0249210.
     17 NOV . 00 . 0008 0249212.
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     17-NOV-2000; 2000US-0249216
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    17-NOV-2000: 2000US-0249245
PR
     17 NoV-2000; 2000US-0249264
PR
     17-NOV-2000; 2000US-0249265.
     17 NoV-2000; 20000S-0249297
     17 NoV-2000; 200005:0249299
PR
PR
     17-NOV-2000; 2000US-0249300
    -01-DEC-2000; 2000US-0250160.
     01 \cdot \text{DEC} \cdot 2000; 200008 \cdot 0250391.
DR
PR
    -0^{4} \cdot DEC \cdot 2000; -20000S \cdot 0251030
    - 05-DEC-2000; 2000US-0251988
PR
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    -08-DEC-2000; 2000US-0251856.
PR
    -08-DEC-2000; 2000US-0251868.
PR
     08-DEC-2000; 2000US-0251869.
     08-DEC-2000; 2000US-0251989.
PR
     08-DEC-2000; 2000US 0251990.
PR
     11-DEC 2000; 2000US-0254097
PR
     -05-JAN 2001; 2001US:0259678
XX
    (HUMA ) HUMAN GENOME SCI INC.
PΑ
XX
     Rosen CA. Barash SC. Ruben SM:
12.1
ХX
     WP1; 2001-465460/50.
DR
     N PSDB; AAS27158.
DR
PT
     Novel polypoptides useful for diagnosing, freating, preventing and/or
     prognosing disorders related to the proteins, including cancers, immune
PT
PT
     disorders and neuronal disorders
ХX
     Claim i; SEQ ID No 806; 880pp; English.
PS
XX
     The invention relates to novel isolated polypeptides (i), and
CC
     polynucleotides (it), (i), (ii) and the antibody to (i) are usetal to
     diagnosing, preventing and treating diseases including immune system
     disorders (e.g. congenital and acquired immonodeficiencies, autoimmune
(1)
     disorders (e.g rhemmatoid arthritis), inflammatory conditions, organ-
    transplant rejections and graft versus host disease, intectious diseases
CC
     (e.g. hepatitis C), bleeding disorders, backooglobin abnormalities and
     other blood related disorders (sickle cell anaemia), myeloproliterative
    disorders, primary haematopoletic disorders, hyperproliterative
    disorders (e.g. Gaucher's disease and cancer), neurodegenerative
    disorders (e.g. Algheimer's disease, Parking m's disease), chromasomai
     abnormalities (Down syndrome), ischaemic injury (e.g. stroke), renal-
     disorders (e.g. glomerulonephritis), cardiovascular disorders
CC
     (e.g. arrhythmia), respiratory disorders, dermatological disorders, in
CC
     wound healing, epithelial cell proliferation, endocrine disorders (e.g.
     Addison's disease), reproductive system disorders, qustrointestinal
00
     disorder (inflammatory disorders), liver disorders (cirrhosis).
     as stimulators of B cell responsiveness to pathogens, activators of
     f-cells, to induce higher affinity antibodies, and as a means to induce
     tumour proliferation in pathologies e.g. acquired immune deficiency
     syndrome (AIDS). AAU17059-AAU17683 represent novel signal transduction
     pathway protein, amino acid sequences of the invention.
ХX
                          -1.9%; Score 10; DB 27; Length 254;
  Best Local Similarity 100.0%; Prod. No. 0.15
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      146 DEKTONIEED 155
      132 diktamilid 14i
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AAB85038
      AAB85038 standard; Protein: 330 AA
      AAB85038;
xx
      06-AUG-2001 (first entry)
\Gamma \in I
XX
DE:
      Human SER4 protein sequence.
хх
      Serine/threshise Finaschike protein; SIRX; broast; testicular; cancer; cardinascular, autoimmune disorder; cytostatic; cardinat; gebe therapy immunosuppressive; antiasthmatic; antifibrinolytic; SER4.
EW
KW
XX
      Homo sapiens.
US
ХX
PN
      W0200136645-A2.
XX
PD
       25-MAY-2001.
ХX
      17 NOV-2000; 2000WO-US31744.
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                          99US-0165986.
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PR
       13-APR-2000; 2000US-0197080.
      15-SEP-2000; 2000US-0232677.
16-NOV-2000; 2000US-0165986.
PR
PR
XX
       (CURA-) CURAGEN CORP.
PA
ХX
       Ouinn KE, Spytek KA, Majumder K, Verret C, Burgess C, Fernandes E;
PI
       Taupier R, Rastelli L, Herrmann JL;
XX
       WPI; 2001-336006/35.
DR
DR
       N-PSDB; AAF83969.
XX
PΤ
       New isoluted SERX polynucleotides and polypeptides related to the
      serine/threenine kinase family of prote ns. useful for determining and treating diseases related to altered levels of the polypeptide -
PΤ
PΤ
XX
PS
       Claim 1: Page 21; 127pp; English.
ХX
CC
       The invention relates to sering/threen to kinase-like proteins, termed
čč
       SERX. The SERX polynucleotides can be used to express SERX protein (e.g.
66
66
66
66
       via a recombinant expression vector in thest cell in gene therapy
      applications), to detect SERX mRNA (e.q in a biological sample) or a genetic lesion in a SERX gene and modulate SERX activity. The SERX polypoptides, polypubleotides, antibodies can also be used to treat or prevent a pathology associated with SERI. Disorders associated with aberrant SERX expression or activity include breast or testicular cancer,
CC
CC
       cardiovascular defect, autoimmune disorders and asthma. Disorders
CC
       associated with aberrant SER5-8 express on include, blood clotting
       hematopoietic and tumor related disorde s. The present sequence
       represents the amino acid sequence of human SER4 protein.
XX
       Sequence 30 AA;
SO
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   Matches 10: Conservative 0; Mismatches 0; Indels 0; Caps 0;
        146 DEKTQNILLD 155
        128 diktqnilld 137
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GenCore version 1 5
                   Copyright (a) 1992 - 2000 tompugen ind
OM nucleic - nucleic search, using sw model
                 May 13, 2002, 19:55.39 , Sea ch time 2937.39 Seconds (without alignments)
Run en:
                                                 9640.059 Million cell updates, see
Title:
                  US-09-445-223-2
Perfect score:
                  2098
Sequence:
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                                                алазлазлазлазлазлазла 2008
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                  Gapop 60.0 , Gapext 60.0
Searched
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Total number of hits satisfying chosen parameters:
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Maximum DB seq length: 2000000000
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                 6: em_estpl:*
                 7: em_estro:*
                 8: em_htc:*
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1): gb_est2:*
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                 16: em_gss_vrt:*
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Pred. No. is the number of results predicted by chance to have a score greater than of equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

			-			SOMMARIES	
Res	ult. No.	Score	* Query Match	Length	DB	ID	Description
	1	693	33.0	811	; 0	N3370405	(e)170405 602322726
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	3	650	31.0	883	1.0	PG393551	BG393551 602411943
	4	598	28.5	1011	1.0	RM469352	BM469352 AGENCOURT
C	C.	642	28.2	E 9.5	Ö	A1745575	A1745575 wc34f12.x
C	6	554	26.4	636	10	BE551615	BE551615 7a42q06.x
	7	551	26.3	912	1.0	RI257472	B1257472 602967861
	8	532	25.4	C15	9	AA160647	AA160647 2449c11.r
C	9	5.30	⇒ E 4	647	Q.	AW960501	AW960501 EST272572
	10	505	24.1	970	1.0	BE877822	BE87/822 601486392
	11	500	23 P	750	1.0	B150000	B1260990 602972155
C	1.2	455	21 7	6.06	- 5	AWORSEO	Αψύ855εύ ωγεί/αύ4 χ
C	1.3	449	21.4	455	4	A1343850	A:343850 qp07401 😿
	1.4	448	21 4	৪৭५	10	R1920776	B182977c e03034378
	15	445	21 2	8 D B	1.0	RF875947	BE875947 601486423
C	16	421	20 2	615	9	AT801150	ATR01150 (085),04 x
C	17	4.2.3	20.2	423	3	AA574167	AA574167 nl78b01.s

C	18	422	20.1	518	9	AW593657	AW593657 x194d07.x
	1.9	122	20.1	641	9	AW150810	AW150819 x439408 x
	20	4.12	19.6	17.7.4	1.0	BM014010	RMO (40) O FORFZORS 3
C	21	411	19.6	4.83	9	AI343247	AI343247 tb94a04.x
c	22	101	19.3	115	13	AW820715	AW820715 RC5-ST030
· ·	23	394	18.8	4.00	9	AA826052	AA826052 od60b09.s
C	24	393	18.7	487	9	AW393452	AW393452 RC5-ST030
	25	5.71	13.6	1656	10	BM468817	BM468817 AGENCOURT
	26	387	18.4	77€	10	BG574192	BC574192 602596077
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C	3.0	370	17.6	446	9	BE002713	BE002713 QV4-BN009
0	3.1	355	16 9	476	C)	AA913804	AA913804 0135dll.s
С	3.2	355	16.9	616	9	AI307810	A1307810 tb28d07.x
e	3.3	353	16.8	445	9	AW820730	AW820730 RC5-ST030
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	4.3	ا الله د	15.5	420	-51	ALCOROGE	ALS98966 DKF2p3131
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C	4.5	419	15.2	493	10	CU5866	C05866 C05866 Huma

ALIGNMENTS

RESULT 1	
BG170405	
LOCUS	BG170405 811 bp mRNA linear EST 06-FEB-2001
	602322736F1 NTH_MGC_99 Homo sapiens GDNA clone IMAGE:4426016 5',
DEPINITION	
	mRNA_sequence.
ACCESSION	BG170405
VERSION	BG170405.1 G1:12677108
KEYWORDS	EST.
SOURCE	human.
ORGANISM	Homo sapiens
	Eukarvota: Motazoa: Chordata, Craniata: Vertebrata: Euteleostomi:
	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE	1 (bases 1 to 811)
AUTHORS	MITH MOTE Strip (1909) in the decay.
Tittle	National Institutes of Health, Mammalian Gene Collection (MGC)
	Unpublished (1999)
TOURNAL	
COMMENT	Contact: Robert Strausberg, Ph.D.
	Email: cgapbs-r@mail.nih.gov
	Tissue Procurement: ATCC
	cDNA Library Preparation: Life Technologies, Inc.
	cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
	DNA Sequencing by: Incyte Genomics, Inc.
	Clone distribution: MGC clone distribution information can be
	found through the CompAction decision (TINE at:
	http://image.llnl.gov
	Plate: LLAM10172 row: q column: 09
	High quality sequence stop: 721.
FEATURES	Longtion/Qualifiers
avutie	1811
.,,,,,,,	/organism "Homo sapiens"
	ide aref "tison: 9606"
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	/Lissur_type "hypernephroma, cell line"
	.dah_host "DH10H (phage-resistant)"
	/sofe-"Organ kidney Vector pCMV SPORT6, Site_1: Not1:
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	Average insert size 1.3 kb. Library enriched for
	full length clones and constructed by Life Technologies.
	Note, this is a NIH_MGC Library."
	•

COMMENT

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BASE COUNT
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CRECTA
     galery Miller
                                                                       33.0%; Source 693; DB 10; Length 811;
     Best Local Similarity [100.0%; Fred. No. 5.2e [5];
     Matches for Conservative 0; Mismatches 0; Indels 0; Gaps
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               LPG at Franquesufetttettaaaatqtttaataqaaetqqaaeeaqttttqaqaeeatttq [1151
                            100
                    • L. AT JAAAGA MATEUTTUUT FAAAATGIJ LAA FAGAAGT FGAAGGAGTTTTGAGAAGATTTG. 129
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               1372 at cut gqt coucaagaagaat cat gt ggat cete teaget eeat gaaaat agt ggt tete - 1331
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Lab
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Lib
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                 4.11 TIPTIGGAPTICAAAGGGCIGGATTITGIGATCACAAGACCACICCATGCTCTTCAGCAA 480
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100
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100
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                          501 AGE GETAGA IGCOCTICTO FORAGOGACT FGATCA IGAAAGAGGACTATGAACTTGTTA 660
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                           THE GLAD CAAGE TRACAAGGACCTECAAAAGTCAGAC 693
RESULT 2
161757472
1 0.11183
                                 n:17574.2
                                                                                                     25-2 bp mRNA
                                                                                                                                                      linear EST 15 MAY 2001
DEPTHUBBLE ON
                                    State of the Nill MGC 18 dismonscriptions of NA clean (IMAGE, 4851542) 5
                                    RNA sequence.
A 1/1ESSS CON-
                                 H 17574.2
VERSION
                                 is1757422.1 GI:14068075
KIDSWORLS:
SHAURCE
                                 E man
    - ORGANISM - s and supiens
                                  Enkaryota; Metazoa; Chordata; Cramiata; Vertebrata; Euteleostomi;
                                  Mammal.a; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
                                         (bases 1 to 852)
     AUTHORS
                                 NOTH MORE But the Commencial Continues as a conti-
                                  Sational Institutes of Health, Mammalian Gene Collection (MGC)
     TITLE
                                   apublished (1999)
     JOHRNAL.
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Email: cgapbs-r@mail.nih.gov
          Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
          cDNA Library Preparation: Ling Hong/Rubin Laboratory
          CDNA Library Arrayed by: The f.M.A.G.E. Consortium (LLNL)
          DNA Sequencing by: Incyte Genomics, Inc.
          Clone distribution: MGC clone distribution intormation can be
          found through the L.M.A.G.E. Consortium/LLNL at:
         http://image.llnl.gov
          Plate: LLCM1694 row: i column: 15
          High quality sequence stop: 814.
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                 Site_2: EcoRI; cDNA made by oligord1 priming.
                 Directionally cloned into EcoRI/Xhol sites using the
                 following 5' adaptor; GGCACGAG(G). Size-selected -500bp
                 for average insert size 1.8kb. Library constructed by Ling
                 Mong in the laboratory of Gerald M. Rubin (University of
                 California, Berkeley) using ZAP cDNA synthesis kit
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                 Note: this is a NIH_MGC Library."
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Db.
    1199 ttacagagtgtttcaggtgccattcacctatgtgacaagaggaaaatggaattatctctg 1258
Οv
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    1259 aagatacctgtaaatcatggtccacaaqaggaatcatgtggatcctct.cagctccatgab 1318
ΟV
        181 AACATACCTGTAAATCATGGTCCACAAGAGGAATCATGTGGATCCTCTCAGCTCCATGAA 240
Db
    1319. aataytyytte teel yaaact kraayyte cel goraye teet caayaraat gät til tita (178
ŲУ
        241 AATAGTGGTTCTCCTGAAACTTCAAGGTCCCTGCCAGCTCCTCAAGACAATGATTTTTTA 300
Db
    1379 tetagaaggeteaggactqttattttatqaagetgeateactqteetqqaaateacagt 1438
QУ
        Db
     301 TCTAGAAAAGCTCAAGACTGTTATTTTATGAAGCTGCATCACTGTCCTGGAAATCACAGI 360
    (14.39) tigagatagoacoaf filotogatoto aaaagga tigoaf fot af aa fa aa aa aacoaotiooa (14.98)
VY
        361 TGGGATAGCACCATTCTGGATCTCAAAGGGCTGCATTCTGTGATCACAAGACCACTCCA 420
Db
    1499 - Egotlet ticageaataataaateeaatti teaactigeaggaaa, ticagaacgtiet geageet - 1558
\nabla \lambda
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Contact: Robert Strausberg, Ph.D.

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VERSION
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 REFERENCE
                                            1 (bases 1 to 883)
                                           NEW MIC Lety //mspc.nc; nih p.//
National Institutes of Health, Mammalian Gene Collection (MGC)
       AUTHORS
       TITLE
        JOURNAL
                                           Unpublished (1999)
 COMMENT
                                             Contact: Robert Strausberg, Ph.D.
                                            Email: cgapbs-r-mail.nih.qov
                                            Tissue Procurement: ATCC
                                              CDNA Library Preparation: Life Lechnologies, Inc.
                                               cDNA Library Arrayed by: The I.M.A.C.E. Consortium (LLNL)
                                            DNA Sequencing by Incyte Genomics, Inc. information can be to md through the I.M.A of F. Conserting Inc. at
                                            http://image.llnl.gov
                                            Plate: LLAM10471 row: e column: 12
                                            High quality sequence stop: 767.
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                                                                            Note: this is a NIH_MGC Library."
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        Ouerv Match.
                                                                                             31.0%; Score 650; DB 10; Length 883;
       Best Local Similarity 100.0%; Pred. No. 4e-141;
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ACCESSION
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VERSION
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REFERENCE
                     1 (bases 1 to 1011) him mil by popular.
   AUCHORS.
                      National Institutes of Health, Mammalian Gene Collection (MGC)
   TITLE
   JOHENAL
                     Unpublished (1999)
                      Contact: Robert Strausberg, Ph.D.
COMMENT
                      Email: cyapbs rimail.nih.gov
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                       cDNA Library Preparation: Lite Technologies. Inc.
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                                              Musmai r. Batheria, Frimates, Catarrhini, Hominidae; Homo.
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      AUTHORS
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                                              Sational Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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                                                charle spapes romaitemik.gov.
                                                 issue Producement: Michael J. Brownstein, M.D., Ph.D., Michael R.
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Emmert-Buck, M.D., Ph.D.
          CDNA Library Preparation: M. Bento Soares, Ph.D.
           CDNA Library Arrayed by: Greg Lennon, Ph.D.
           DNA Sequencing by: Washington University Genome Sequencing Center
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     Db
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1010
    1517. aatocacticticaactycaggaaacticagaacytictycagcctygtatagcccagcagtgu. 1576
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VERSION
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REFERENCE
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                       National Cancer Institute, Cancer Genome Anatomy Project (CCAP).
    LITLE
                       lumor Gene Index
    TOTIENAL
                      Unpublished (1997)
 COMMENT
                       Contact: Robert Strausberg, Ph.D.
                       Email: cgapbs-remail.nih.gov
                       lissue Procurement: Christopher r. Moskaluk, M.D., Ph.D., Michael
                       R. Emmert-Buck, M.D., Ph.D.
                        CDNA Library Preparation: M. Berto Soares, Ph.D., M. Fatima
                       Bonaldo, Ph.D.
                        CDNA Library Arrayed by: Greg Lennon, Ph.D.
                        DNA Sequencing by: Washington University Conome Sequencing Center
                        Clone distribution: NCI-CGAP clone distribution information can be
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/note="Yector: pT7T3D-P.c (Pharmacia) with a modified polylinker: Site_1: Not I; Site_2: Ecc RI; Plasmid DNA from the normalized library NCI_CGAP_SC4 was prepared, and
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                                       this DNA was used as trucer in a subtractive hybridization reaction. The driver wa: PCR-amplified cDNAs from a pool
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                                       Subtraction by Bento Source and M. Fatima Bonaldo.
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            494 IGATCA/AAGACCACTCCATGC1CTTCAGCAA1AAIAAAGCCACTCTCAACTGCAGGAAA 435
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          1540 Cticaqaacqtetucagectuqtataqcccaqeaqiggaticcaqaacaaqqqaagacat 1599
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      314 CLIGATEA GAAAGAGGA TATGAA ETIGITAGTAG AAG CTACAAGGACTCAAAAGT 255
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          74 AGAAA IGTGTI ICATAAAAGGATAI TIATATCTCI GTTGCI I IGACTTTTTTTATATAAA 15
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          . [3] [4] [4] [4]
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       14 ATCCCTGAGTATTA 1
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 AUTHORS
           NIH-MGC http://mqcinci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
  TITLE
  JOHRNAL
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COMMENT
            Contact: Robert Strausberg, Ph.D.
            Email: eqapbs-r mail.bib gov.
            Tissue Procurement: ATCC
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           Manumalia: Eutheria: Primates: Catarrhini: Hominidae: Homo.
           . (bases 1 to 645)
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           Stiller, L., Lennon, G., Recker, M., Bonaldo, M.F., Chiapelli, R.,
           Thissee, S., Dietrich, N., Dabaque, L., Faveilo, A., Gish, W., Hawkins
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           Seneration, and analysis of 280,000 human expressed sequence tags
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           Terraine Rest. 6 (3), 807 828 (1996)
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           444 8
 MMENT
           Cartach , William RK
           washington University School of Medicine.
           3444 Forest Park Parkway, Box 8501, St. Louis, Mo 63108
           sels 314 286 1800
           -ax: 314 286 1810
           smail. est watson.wastl.edu-
           his come is available royalty free through LLNL, contact the
           MAGE Insortium (intodinage, iln., gov) for further information.
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                    Legder F. Oi.R., Abernathy, K., Erarap, S., Caspard, R., Gay, C., Holt , I.E., Saeed, A.1., Sharov, V., Lee, N.H., Yeatman, F.J. and
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                     The Institute for Genomic Research
                     9712 Medical Center Dr., Rockville, MD 20850, USA
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                     Fax: 301 838 0208
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REFERENCE
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REFERENCE
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 JOURNAL.
COMMENT
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           Email: egaphs-remail.nih.gov
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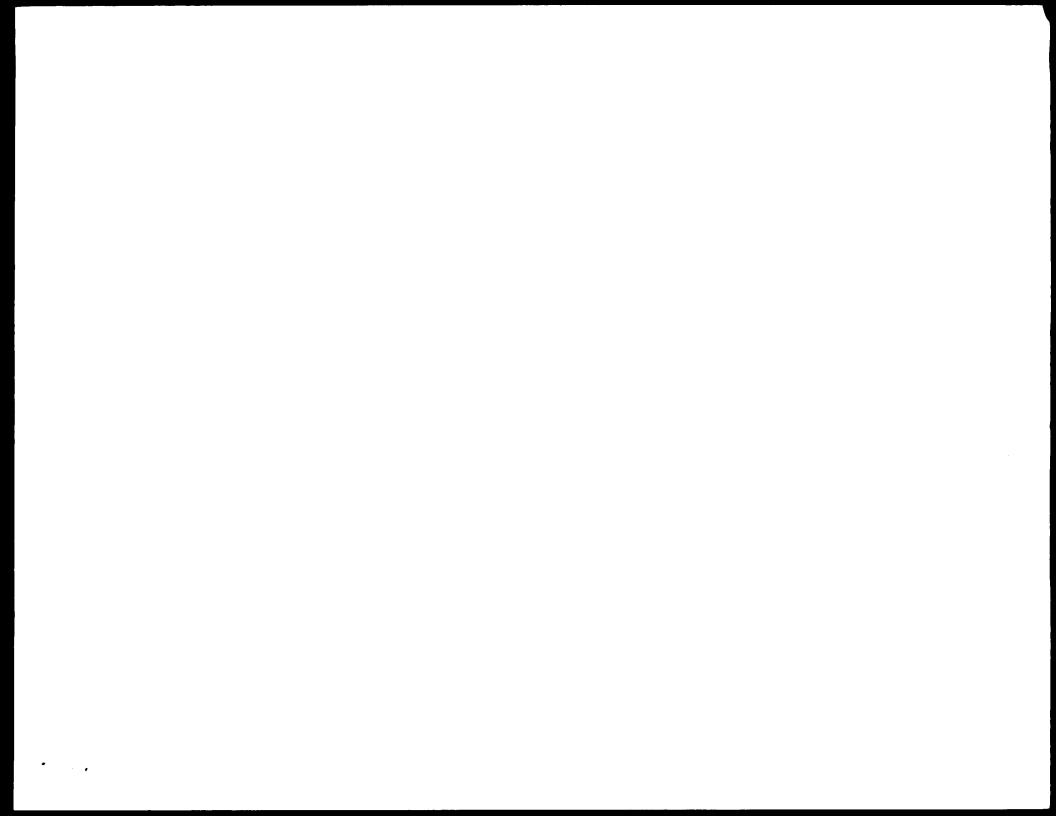
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 REFERENCE
                          NIH Mele http://meg.land.mah.epo./c
    AUTHORS
    11111
                          National institutes of Health, Mammailian Some Collection (MGC)
     J OFFNAL.
                          Unpublished (1999)
                          Contact: Robert Strausberg, Ph.D.
 CHMMENT
                          Email equiples romail.nih.gov
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                           CONA Library Preparation: Life Technologies, Inc.
                            CONA Library Arrayed by: The L.M.A.G.E. Consortium (LLNL)
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REPERENCE
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COMMENT
          Contact: Robert Strausberg, Ph.D.
           Email: cgapbs:r-mail.nih.gov
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	1416	67.5	1620	4	US 09 099-0414 3	Sequence 3, Appli
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7	3.7	1.8	880	- 3	US 09-054-298-7	Sequence 7, Appli
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27	3.5	1.7	2469	4	US 09 111 73> 5	Sequence 5, Appli

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	31	3.5	1.7	5852	1	US-U7 867-106-2	Sequence 2, Appli
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ALIGNMENTS

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: Patent No. 6033855
; GENERAL INFORMATION:
     APPLICANT: Bertin, John
      TITLE OF INVENTION, COUNCE ENGAGING CASPASE REORGITMENT THREE OF INVENTOR OF THE PROPERTY OF S
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      Abbresept Put Allers:
Abbresept Pick & Richardson P.C.
Stoppi 2005 Planklin Street
        C'IY: Boston
        STATE: MA
COUNTRY: USA
        ZIP: 02110-2804
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        FILING DATE: 06 FEB-1998
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     ATTORNEY/AGENT INFORMATION:
     NAME: Melklejohn, Ph.D., Anita L.
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TELEPOMMUNICATION INTOMATION:
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; Sequence 1, Application USZ09099041A
, Patent No. 6340576
: GENERAL INFORMATION:
; APPLICANT: Bertin, John
  TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD RELATED
  TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF
: FILE REFERENCE: 07334:076001
  CURRENT APPLICATION NUMBER: 08/09/099,041A
  CURRENT FILING DATE: 1998 06:17
  PRIOR APPLICATION NUMBER: 09/019,942
  PRIOR FILING DATE: 1998-02-06
  NUMBER OF SEC 15 NOS: 37
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: SEQ ID NO I
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; Sequence 2, Application US/09069023A
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; Patent No. 6:48573

; GENERAL INFORMATION:

: APPLICANT: Nunez, dabriel

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    APPLICANT, Koseki, Takeyoshi
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     NUMBER OF THE HE NORT OR
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      TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD RELATED
       TIPLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF
       FILE REFERENCE: 07334-076001
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      CURRENT FILING DATE: 1998-06-17
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       PRIOR FILING DATE: 1998-02-06
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               \{\hat{P}_i^{\dagger}P_i^{\dagger}P_i^{\dagger}P_i^{\dagger}P_i^{\dagger}P_i^{\dagger}P_i^{\dagger}P_i^{\dagger}P_i^{\dagger}P_i^{\dagger}P_i^{\dagger}P_i^{\dagger}P_i^{\dagger}P_i^{\dagger}P_i^{\dagger}P_i^{\dagger}P_i^{\dagger}P_i^{\dagger}P_i^{\dagger}P_i^{\dagger}P_i^{\dagger}P_i^{\dagger}P_i^{\dagger}P_i^{\dagger}P_i^{\dagger}P_i^{\dagger}P_i^{\dagger}P_i^{\dagger}P_i^{\dagger}P_i^{\dagger}P_i^{\dagger}P_i^{\dagger}P_i^{\dagger}P_i^{\dagger}P_i^{\dagger}P_i^{\dagger}P_i^{\dagger}P_i^{\dagger}P_i^{\dagger}P_i^{\dagger}P_i^{\dagger}P_i^{\dagger}P_i^{\dagger}P_i^{\dagger}P_i^{\dagger}P_i^{\dagger}P_i^{\dagger}P_i^{\dagger}P_i^{\dagger}P_i^{\dagger}P_i^{\dagger}P_i^{\dagger}P_i^{\dagger}P_i^{\dagger}P_i^{\dagger}P_i^{\dagger}P_i^{\dagger}P_i^{\dagger}P_i^{\dagger}P_i^{\dagger}P_i^{\dagger}P_i^{\dagger}P_i^{\dagger}P_i^{\dagger}P_i^{\dagger}P_i^{\dagger}P_i^{\dagger}P_i^{\dagger}P_i^{\dagger}P_i^{\dagger}P_i^{\dagger}P_i^{\dagger}P_i^{\dagger}P_i^{\dagger}P_i^{\dagger}P_i^{\dagger}P_i^{\dagger}P_i^{\dagger}P_i^{\dagger}P_i^{\dagger}P_i^{\dagger}P_i^{\dagger}P_i^{\dagger}P_i^{\dagger}P_i^{\dagger}P_i^{\dagger}P_i^{\dagger}P_i^{\dagger}P_i^{\dagger}P_i^{\dagger}P_i^{\dagger}P_i^{\dagger}P_i^{\dagger}P_i^{\dagger}P_i^{\dagger}P_i^{\dagger}P_i^{\dagger}P_i^{\dagger}P_i^{\dagger}P_i^{\dagger}P_i^{\dagger}P_i^{\dagger}P_i^{\dagger}P_i^{\dagger}P_i^{\dagger}P_i^{\dagger}P_i^{\dagger}P_i^{\dagger}P_i^{\dagger}P_i^{\dagger}P_i^{\dagger}P_i^{\dagger}P_i^{\dagger}P_i^{\dagger}P_i^{\dagger}P_i^{\dagger}P_i^{\dagger}P_i^{\dagger}P_i^{\dagger}P_i^{\dagger}P_i^{\dagger}P_i^{\dagger}P_i^{\dagger}P_i^{\dagger}P_i^{\dagger}P_i^{\dagger}P_i^{\dagger}P_i^{\dagger}P_i^{\dagger}P_i^{\dagger}P_i^{\dagger}P_i^{\dagger}P_i^{\dagger}P_i^{\dagger}P_i^{\dagger}P_i^{\dagger}P_i^{\dagger}P_i^{\dagger}P_i^{\dagger}P_i^{\dagger}P_i^{\dagger}P_i^{\dagger}P_i^{\dagger}P_i^{\dagger}P_i^{\dagger}P_i^{\dagger}P_i^{\dagger}P_i^{\dagger}P_i^{\dagger}P_i^{\dagger}P_i^{\dagger}P_i^{\dagger}P_i^{\dagger}P_i^{\dagger}P_i^{\dagger}P_i^{\dagger}P_i^{\dagger}P_i^{\dagger}P_i^{\dagger}P_i^{\dagger}P_i^{\dagger}P_i^{\dagger}P_i^{\dagger}P_i^{\dagger}P_i^{\dagger}P_i^{\dagger}P_i^{\dagger}P_i^{\dagger}P_i^{\dagger}P_i^{\dagger}P_i^{\dagger}P_i^{\dagger}P_i^{\dagger}P_i^{\dagger}P_i^{\dagger}P_i^{\dagger}P_i^{\dagger}P_i^{\dagger}P_i^{\dagger}P_i^{\dagger}P_i^{\dagger}P_i^{\dagger}P_i^{\dagger}P_i^{\dagger}P_i^{\dagger}P_i^{\dagger}P_i^{\dagger}P_i^{\dagger}P_i^{\dagger}P_i^{\dagger}P_i^{\dagger}P_i^{\dagger}P_i^{\dagger}P_i^{\dagger}P_i^{\dagger}P_i^{\dagger}P_i^{\dagger}P_i^{\dagger}P_i^{\dagger}P_i^{\dagger}P_i^{\dagger}P_i^{\dagger}P_i^{\dagger}P_i^{\dagger}P_i^{\dagger}P_i^{\dagger}P_i^{\dagger}P_i^{\dagger}P_i^{\dagger}P_i^{\dagger}P_i^{\dagger}P_i^{\dagger}P_i^{\dagger}P_i^{\dagger}P_i^{\dagger}P_i^{\dagger}P_i^{\dagger}P_i^{\dagger}P_i^{\dagger}P_i^{\dagger}P_i^{\dagger}P_i^{\dagger}P_i^{\dagger}P_i^{\dagger}P_i^{\dagger}P_i^{\dagger}P_i^{\dagger}P_i^{\dagger}P_i^{\dagger}P_i^{\dagger}P_i^{\dagger}P_i^{\dagger}P_i^{\dagger}P_i^{\dagger}P_i^{\dagger}P_i^{\dagger}P_i^{\dagger}P_i^{\dagger}P_i^{\dagger}P_i^{\dagger}P_i^{\dagger}P_i^{\dagger}P_i^{\dagger}P_i^{\dagger}P_i^{\dagger}P_i^{\dagger}P_i^{\dagger}P_i^{\dagger}P_i^{\dagger}P_i^{\dagger}P_i^{\dagger}P_i^{\dagger}P_i^{\dagger}P_i^{\dagger}P_i^{\dagger}P_i^{\dagger}P_i^{\dagger}P_i^{\dagger}P_i^{\dagger}P_i^{\dagger}P_i^{\dagger}P_i^{\dagger}P_i^{\dagger}P_i^{\dagger}P_i^{\dagger}P_i^{\dagger}P_i^{\dagger}P_i^{\dagger}P_i^{\dagger}P_i^{\dagger}P_i^{\dagger}P_i^{\dagger}P_i^{\dagger}P_i^{\dagger}P_i^{\dagger}P_i^{\dagger}P_i^{\dagger}P_i^{\dagger}P_i^{\dagger}P_i^{\dagger}P_i^{\dagger}P_i^{\dagger}P_i^{\dagger}P_i^{\dagger}P_i^{\dagger}P_i^{\dagger}P_i^{\dagger}P_i^{\dagger}P_i^{\dagger}P_i^{\dagger}P_i^{\dagger}P_i
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Db
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ÐЬ	601	gyadaaaaatcaaggydcagtalcaagcacyatatatatagetatgdagttatdaaatgd	660
Qγ	920	gaagtgt.tatccagaaaacagooffffgaagatgtcaccaat.cofft.gcagatatgtat	979
bb	661		720
Оy	980	agtgtgtcacaaggacatcgacctgttattaatgaagaaagtttgccatatgatatacct	10 19
iъb	721		780
ΨY	104-4	caccyaucacytatuatis tetaatauaaytyuutyuucacaaaticagatuaaaya 	1099
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Qy	1160	acttttctrgaagelgttatteagetaaugaaaacuaagttacagaatgttteaagtgee 	1219
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ψy	1220	afts acctafqfqa aggaaqaaantqqaattats istgaacafaccfqfaatcctqqf 	1279
1915	961		1020
Qÿ	1280	crasaagaqqaatsatgtqqatsststaaqetssatqaaaataqtqqttctcctqaaact }}	1339
Db	1021		1080
Qγ	1340	Leaaggteectgeeageteeteagaeaatgattiittitatetagaaaageteaagaetgt	1399
Db		t dáággítt er tyccagott ritt adjacaat gatt titt tallet agádaáge teáagás tuti	
Qγ		-faffftätgaagcfgcatcactgfcctggaaafcacagffgggafagcaccaffttötgga -[}	
dd	1141	taltttatquagetqeateactqt.cctqquaaateacaqttqqqaataqeaceattt.ctqqu	1200
Qу	1460	teleaaaqqqetgeattelqtgafeacaaqaceacteeatgeletteaqcaataataat 	1519
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Qу		qatqccctfctqfccaqqqactfqatcatqaaaqaqactatqaactfdttaqtaccaaq 	
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Qy		ccqqaaafacttqtqqt!fctqqafcaccatcftfaaaftEacttcaaaataaaaqcafq -{ }	
Ob	1561	ceggaaataettgtggfftctagateaecatefffaaattla-fftSääaätääääägdatg	1620

RESULT 5 US-08-700 575-31

: Sequence 41, Application US/08700575

; Patent No. 5817479

```
TENERAL NERMALISM:
    APPLICANI: Au Young, lamice
    APPLICANCE Randman, Olique
    APPLICANT: Bawkins, Phillip R
APPLICANT: Wolder Craig 5.
    FILLE & INVENTION: NOVEL BOMAN KINADE DEMONSOR
     NUMBER I SEQUENCES: 45
      THRREST NORMOR ADDRESS:
      ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
      STREET SOME PORTER DRIVE
       TOTY PALL ALLY
       TOUNTRY 1.3A
       Z4P: 94304
      MEUTER REALARLE FORM.
       MEDICM TYPE - Floppy disk
       COMPULER: IBM PC compatible
       PERALING SYSTEM: PC DOS/MS DOS
       SOFTWARE: Futentin Release #1.0, Version #1.00
     CURRENT APPLICATION DATA:
      APPLICATION NUMBER: 007/08/27 - ,575
      FILIST DATE
      STLASS SELECTATIONS 435
     ALIDENI (ZAGEN) INDERMALION.
      NAME BILLINGS, LUCY L
       REGI. RATION NUMBER: 06749
      MERENDATE/A - "KIT NUMBER, OF 100 US
     TELECOMMUNICATION INFORMATION:
      TELEFO NET 415 855 0505
      TELEFAX: 415 845 4166
   INFORMATION FOR SEQUED NO. 31
    CHOCLENGS THARACTERISTIC'S:
      LENGIN: 21 - base pairs
      TYPE machine acid
       MIRAN ELNEST: single
      Letorety: cinear
     MODERBUL EVEL CHINA
     IMMEDIA E SCUSSE:
      STBRASY. THE I Phorbot LPS.
10NF 15610B
                       10.0%; Scare 210; DB 1; Length 210;
  Rest nord, Similarity 100,0%; Fred, No. 5, 3e 80;
  Matches z: (; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
      384 - turrinaet iitgaacet ogacaaaaat caaqqeecaqtat caaqeaacqatatatatatageta. 983
         I TORANACIA (GARCEGOACANAA CANAGOGOCAGIA CANGCAGATATATATATAGOIA 60
      .c.4. tu. lig?ta?cacatququaqtqftatccuqaaalcaqccttffq&aqufqfcacceatcc.963

    Enditablea i racia (gagaag egilta egirada adada egibt endaaga egibtactaa rect. 120)

      .e.4. tt: prigataatgtatagtgtgtcacaaggacatcgacctgttattaatgaagaaagttt. 1023
         ar sais esiminisimo illo si objenimistimisti
      ...! re spaga (anigualagi) gugu baranga panga pangalagi ataa isaagaagaagtil 180
     3624, qc. at at gat at and cannigagoacquart 1053.
         [10] J. B. Marchard, Phys. Lett. B 50 (1994).
      Les de Asaldasalamentetadesadetadiai ele
832001 F
113 OB F. 6 36-A C
 Geoplemore, 7 = App_{\rm FB} but for USZCB616308A statem. No. . . . 9.726\%
  CHENERAL INFORMATION.
    Aller P'Able Bees Mir Ein-
    Alli C'Abd Horer, Edgir
    - Akirkur'Ahori - Barno Mukeshi
   APPL CANTE YET, Shaw Fang
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```
TIBLE OF INVENTION: SMOOTH MUSICE CELL LIM PROTEIN
    NUMBER OF SEQUENCES: 40
    CORRESPONDENCE ADDRESS:
     ADDRESSEE: Fish & Richardson P.C.
      SIREET: 22% Franklin Street
      CITY: Boston
      STATE: MA
     COUNTRY: USA
      ZIP: 02110 2804
    COMPUTER READABLE FORM:
      MEDIUM TYPE: Floppy disk
      COMPUTER: IBM PC compatible
      OPERATING SYSTEM: PC-DOS/MS-DOS
      SOFTWARE: Patentin Release #1.0, Version #1.30
    CURRENT APPLICATION DATA:
      APPLICATION NUMBER 100/08/616,368A
      FILING DATE: 15 MAR-1996
     CLASSIFICATION: 514
    ATTERNEY/AGENT INFORMATION:
     NAME: Fraser, Jamis K.
      REGISTRATION NUMBER: 34,819
      REFERENCE/DESCRET NUMBER: 054/03/2001
    TELECOMMUNICATION INFORMATION:
     TELEPHONE: 617/542-5070
      TELEFAX: 617/542 8906
     TELEX: 200154
; INFORMATION FOR SEQ ID NO: 7:
   SEQUENCE CHARACTERISTICS:
     LENGIH: 880 base pairs
      TYPE: mucleic acid
     STRANDEDNESS: both
     ToPotoGY: Linear
   MOLECULE TYPE: DNA
US-08 616-368A 7
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 Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps
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        RESULT 7
US 09:054-298:7
; Sequence 7, Application US/09054298
; Patent No. 6136953
; GENERAL INFORMATION:
   APPLICANT: Lee, Mu En
    APPLICANT: Haber, Edgar
    APPLICANT: Jain, Mukesh
    AFFLICANT: Yet, Shaw Fang
    TITLE OF INVENTION: SMOOTH MUSCLE CELL LIM PROTEIN
    NUMBER OF SEQUENCES: 40
    CORRESPONDENCE ADDRESS:
     ADDRESSEE: Fish & Richardson P.C.
      STREET: 225 Franklin Street
     CITY: Boston
      STATE: MA
     COUNTRY: USA
      ZIP: 02110 2804
    COMPUTER READABLE FORM:
      MEDIUM TYPE: Diskette
     COMPUTER: IBM Compatible
     OPERATING SYSTEM: Windows 95
      SOFTWARE: FastSEQ for Windows Version 2.0b
    CURRENT APPLICATION DATA:
      APPLIETATIEN NUMBER: TUJOGJO54.298
     FILING DATE: 02 APR-1998
    PRIOR APPLICATION DATA:
      APPLICATION NUMBER: 08/616,368
```

STRANDEDNESS: both

```
FILING DATE: 15-MAR-1996
    AITORNEY/AGENT INFORMATION.
      NAME: Beattie, Ph.D., Ingrid A.
      REGISTRATION NUMBER: 19-42,206
REFERENCE,CASTEET NUMBER: 05433/022002
     TELECOMMUNICATION INFORMATION:
      TELEPHONE: 617/542-5070
      TELEFAX: 617/542-8906
       TELEX: 200154
  INDERMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
      LENGIH: 880 base pairs
      TYPE: nucleic acid
      STRANDFONESS: both
      TOPOLOGY: linear
    MOLECULE TYPE: DNA
    FEATURE:
      NAME/KEY: Coding Sequence
      LOCATION: 55. .633
US-09-054-298-7
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    2062 atttqaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaa 2098
        RESULT 8
US-08-818-655-7
; Sequence 7, App.ication US/08818655
; Patient No. 6258557
: GENERAL INFORMATION:
    APPLICANI: Lee, Mu-En
    APPLICANI: Haber, Edgar
    APPLICANT: Jain, Mukesh
    APPLICANT: Yet, Shaw-Fang
    TITLE OF INVENTION: SMOOTH MUSCLE CELL LIM PROTEIN
    NUMBER OF SEQUENCES: 46
    CORRESPONDENCE ADDRESS:
      ADDRESSEE: Fish & Richardson, P.C.
      SIMBET: 225 Franklin Street
      CITY: Boston
      STATE: MA
      COUNTRY: US
      ZIP: 02110-2804
    COMPUTER REAL-ABLE FORM:
      MEDIUM TYPE: Diskette
      COMPUTER: IBM Compatible
      OPERATING SYSTEM: Windows95
       SOFTWARE: FastSEQ for Windows Version 2 0
    CURRENT APPLICATION DATA:
      APPLICATION NUMBER 03,708,7818,655
      FILING DATE: 14-MAR-1997
      CLASSIFICATION: 514
     PRIOR APPLICATION DATA:
      APPLICATION NUMBER: 08/616,368
      FILING DATE: 15-MAR-1996
    ATTORNEY/AGENT INFORMATION.
      NAME: Fraser, Janis K.
       REGISIRATION NUMBER: 34,819
       REFERENCE, TOCKET NUMBER: 05433, 4040001
     TELECOMMUNICATION INFORMATION:
      TELEPHONE: 617 542-5070
TELEFAX: 617-542-8906
   INFORMATION FOR SEC 1D NO. 7.
     SEQUENCE CHARACTERISTICS:
      LENGTH: 880 base pairs
       TYPE: nucleic acid
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TOPOLOGY: Linear
    MOLECULE TYPE: DNA
    FEATURE:
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LOCATION: 55...64
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US-07-846-992-1
; Sequence 1, Application US/07846992
; Patent No. 5583046
; GENERAL INFORMATION:
    APPLICANT: Valenta, Rudoli
    APPLICANT: Dachene, Michael
APPLICANT: Pettemburger, Karin
APPLICANT: Breitenbach, Michael
     APPLICANT: Kraft, Dietrich
    APPLICANT: Rumpoid, Helmut
APPLICANT: Scheiner, ofto
     TITLE OF INVENTION: Birch Pollen Allergen Fi4 for Diagnosis
     TITLE OF INVENTION: and Therapy of Allergic Diseases
     NUMBER OF SEQUENCES: 11
     CORRESPONDENCE ADDRESS:
      ADDRESSEE: Pennie & Edmonds
       STREET: 1155 Avenue of the Americas
       CITY: New York
      STATE: New York
       COUNTRY: U.S.A.
       ZIP: 10036 2711
     COMPUTER READABLE FORM:
       MEDIUM TYPE: Floppy disk
       COMPUTER: IBM PC compatible
       OPERATING SYSTEM: PC DOS/MS-DOS
       SOFTWARE: Patentin Release #1.0, Version #1.25
     CURRENT APPLICATION DATA:
      APPLICATION NUMBER: US/07/846,992
      FILING DATE: 19920606
       CLASSIFICATION: 435
     PRIOR APPLICATION DATA:
      APPLICATION NUMBER: US 07/354,844
       FILING DATE: 18 MAY 1992
     ATTORNEY, AGENT INFORMATION:
      NAME: Jones III, Harry C
       REGISTRATION NUMBER: 20,280
       RESERVED, DECERT NUMBER: 6530:011
     TELECOMMUNICATION INFORMATION:
      TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-8864/9741
       TELEX. 66141 PENNIE
   INFORMATION FOR SEQ ID NO: 1:
    SEQUENCE CHARACTERISTICS:
      LENGIH: 700 base pairs
       TYPE: NUCLETC ACID
       SIEANCECHESS: single
      TOPOLOGY: linear
     MOLECULE TYPE: CDNA
     HYPOTHETICAL: NO
     ANTI SENSE: NO
    ORIGINAL SOURCE:
     ORCANISM: Botula elimeosa
     IMMEDIATE SOURCE:
US-07-846-992-1
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    Bost Feal amilarity [100,0%; Prod. No. 2,60,06;
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APPLICANI: Dallone, Michael
          ARTITIANI: Pettenburger, Karin
          APPELL'ANCE Proctembach, Michael
          ALI III-'AN
                                 - Krift, Dietrich
          APrilia AN.: Europold, Helmut
          About CANCE Scheiner, Otto-
          TIBLE OF INVENTION: Birch Poller Allergen P14 for Diagnosis
          TIBLE OF INVENTION: and therapy of Allergic Diseases.
          NUMBER - SEQUENCES: II
            TOURESPE GENERAL ADJUNCTION
              AddREC MEET Committee & Edmonds
CORRECT 1155 Avenue of the Americas
                THEY: NOW YORK
                CLATE New York
               COMPUTER REALARDE FORM:
              MEDIUM TYPE: Ploppy disk
               Compute Recognition of Computable
               GERALINI SYSTEM. BY DESZMS LESS
               J. FIWA:F. Fitentin Release #1.8, Version #1.25
            TURRENT MILLIAND N DATA.
              APPLICATION NUMBER: ME, ME, MB, 4100, 151
              TELLING DATE: OF JUN 1995.
                NASSTERCATE NEW 185
          THE OF ALL LOCALD IN DATA:
              APPLICATION NUMBER: 08/01/846.30.
              ETHING DATE: 06 JUN 1902
              APPLICATION NUMBER: US/07/354.844
             FILLING DATE: IB MAY 1992
          ALL FINEY (A JEN) INFORMATION:
              NAME: Comes III, Harry C.
              BECISCRALION NUMBER: 20,280
              REPERENCE/DOORED NUMBER: 6530 011
          TELECOMMINISTATION INFORMATION:
              TELEPH NE: (212) 790 9090
              IFLEFAX: (. 2) 869 8864/9741
IELEX > 614 FENNIE
       TNE HEMALD N FOR JEG ID NOT 1:
         SUQUENCE THARATTERESTICS.
             LisNOTE 700 base pairs
              SYPE: code a acid
              STEAN: INES: single
               a 990La Y. Tamear.
          MELECULE TYPE: CONA
          HYPERIHELL 'ALC: NO
          AND USED UP 1 N
          SELECTIONAL SECURICIES
              - PGAN, IM. - Perbula Verrucosa.
          TMMISSIA : SOUR TES
             TITURALI. PELIEN FROM ALLERGON AB, ENGELHOLM, SWEDEN
2010 OR 4+9-551-1
    generally Mattern
                                                       1.7%, School (F. 1961, Length 700;
     Best Local Similarity 100.0%; Fred. No. 2.56 06;
```

```
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps
gy 2063 Iffqaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaa 2098
        RESULT 11
(JS^{-1})(38^{-1})(34-4^{\frac{1}{4}})(9-5)
; Sequence 5, Application US/08504459
; Patent No. 5922564
; GENERAL INFORMATION:
    APPLICANT: Alderete, John F.
    TITLE OF INVENTION: Adhesin denes and Proteins Involved in
    TIPLE OF INVENTION: Trichomonas Vaginalis Cytoadherence
    NUMBER OF SEQUENCES: 30
    CORRESPONDENCE ADDRESS:
      ADDREDGED. Arnold, White & Durkee
      STREET: P.O. Box 4433
      CITY: Houston
      STATE: Texas
      COUNTRY: US
      ZIP: 77210
    COMPUTER READABLE FORM:
      MEDIUM TYPE: Floppy disk
      COMPUTER: IBM PC compatible
      SPIRATING SYSTEM. FO LOSIMS DOS
      SOFTWARE: Patentin Release #1.0, Version #1.40
    CURRENT APPLICATION DATA:
      APPLICATION NUMBER: US;/08,/504,459
      FILING DATE: Concurrently herewith
      CLASSIFICATION: 435
    ALTORNEY/AGENT INFORMATION:
      NAME: Wilson, Mark B.
      REGISTRATION NUMBER: 37,259
      REPERENCE/SECTED NUMBER: UTSELET NUMBER:
    THILL COMMUNICATION INFORMATION:
     TELEPHONE: 512/418-3000
      IELEFAX. 512/474 7577
      TELEX: N/A
  INFORMATION FOR SEQ ID NO: 5:
    SEQUENCE CHARACTERISLICS:
     LENGTH: 1804 base pairs
      TYPE: nucleic acid
      STRANDEDNESS: single
     ToPOLOGY: linear
    MOLECULE TYPE: other nucleic acid
     DESCRIPTION: /desc "DNA"
    FEATURE:
      NAME/KEY: CDS
     LOCATION: 14..1714
US 08 504 459-5
                       - 1.7%; Score 36; DB 2; Length 1804;
 Best Local Similarity 100.0%; Pred. No. 2.4e 06;
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps
    2064 tttqaaaaaaaaaaaaaaaaaaaaaaaaaaaaa 2098
         Db 1745 LETGAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1780
RESULT 12
US 09 468 590-1
; Sequence 1, Application US/09368590
; Patent No. 618756+
; GENERAL INFORMATION:
; APPLICANT: Solimena, Michele
: TIBLE OF INVENTION: INTERACTING POLYPEPTIDES FOR
  TITLE OF INVENTION: AUTOANTIGENS OF AUTOIMMUNE DISEASES
: FILE REFERENCE: 101918 200 (OCR: 941)
: CURRENT APPLICATION NUMBER: US/09/368,590
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; CURRENT FILING DATE: 1999-08-04
; EARLIER APPLICATION NUMBER: 60/005,657
   EARLIER FILING DATE: 1998-08-07
   NUMBER OF SEQ ID NOS: 8
   SOFTWARE: FastSEQ for Windows Version 3.0
 SEO ID NO I
   LENGTH: 7812
   TYPE: DNA
   ORGANISM: Haman
   FEATURE:
   NAME,/KEY . TLS
   LOCATION: (1)...(6879)
   NAME/KEY: unsure
   LOCATION: (10b)...(102)
   NAME/KEY: unsure
   LOCATION: (1021)...(1023)
   NAME/KEY: unsure
   LOCATION: (2266)...(2268)
US-09-368-590 i
 Ouery Match 1.7%; Score 36; 18 4; Longth 7812, Best Local Similarity 100.0%; Pred. No. 1.1e-66;
 Matches 36; Conservative 0, Mismatches 0, Indels 0, Gaps
    7768 tituaaaaaaaaaaaaaaaaaaaaaaaaaaaaaa 7803
RESULT 13
US-09:592 891A 8
p Gequence 8, Application US/09592891A
1 Patent No. 6329174
: GENERAL INFORMATION.
: APPLICANT: Xiao-Zhou Michelle Wang
  APPLICANT: Xavier Georges Sarda
 APPLICANI: Michael David Tomalski
  APPLICANT: Vincent Paul Mary Wingate
   TILLE OF INVENTION: Heliothis Glutamate Receptor
   FILE REFERENCE: A32815 072667.0118
   CURRENT APPLICATION NUMBER US MAJE 42, 891A
   CURRENT FILING DATE: 2001-01-22
   NUMBER OF SEC ID NOS: 14
  SOFTWARE: FastSEQ for Windows Version 3.0
 SEC 1D NO 8
; LENGTH: 1052
   TYPE, DNA
   ORGANISM: Heliothis virescens
US-09-592-891A-8
 Query Match 1.7%; Score 35; 18 4; Length 1052; Best Local Similarity 100 0%; Pred. No. 6.6e-06;
  Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps
Qy 2064 tiqahaaaaaaaaaaaaaaaaaaaaaaaa 2098
         1017 ttyaaaaaaaaaaaaaaaaaaaaaaaaaaaaaa 1051
RESULT 14
US-09-412-102 3
; Sequence 3, Application US/09412102
; Patent No. 6228992
; GENERAL INFORMATION:
    APPLICANT: JESSEN, HOLLY J
APPLICANT: MEYER, TERRY E
    THILE OF INVENTION: GENES AND METHODS FOR CONTROL OF
    TITLE OF INVENTION: NEMATODES IN FLANTS NUMBER OF SECTENCES: 10
    CORRESPONDENCE ADDRESS.
      ALDRESSEE: W. Murray Spruill (Alston & Bird, LLP)
```

```
STREET: 3605 Glenwood Ave. Suite 310
      CITY: Raliegh
      STAIE: NO
      COUNTRY: US
      ZTP: 27622
    COMPUTER READABLE FORM:
      MEDIUM TYPE: Ploppy disk
      COMPUTER: IBM PC compatible
      SPERATING SYSTEM. FC DOS/MS-DOS
      SOFTWARE: Patentli Release #1.0, Version #1 40
    CURRENT APELICATE & LATA:
     APPLICATION NUMBER: 98/09/412:102
      FILING DATE:
     CLASSIFICATION:
    PRIOR APPLICALL N DATA:
     APPLICATION NUMBER: 09/217,787
      FILING DATE:
    ATTORNEY, AGENT THE RMATE NO
      NAME: Spruill, W. Murray
      REGISTRATION NUMBER: 32,943
       REFERENCE, DOCKEL NUMBER: 5718-18P1
    TELECOMMUNICATION INFORMATION:
      TELEPHONE: 919 420 2202
      TELEFAX. 919 831 4175
  INFORMATION FOR SEQ ID NOT
    SEQUENCE CHARACTERISTICS:
     LENGTH: 1325 base pairs
      TYPE: nucleic acid
      STRANDEDNESS: single
      TOPOLOGY: linear
    MOLECULE TYPE: CDNA
    ORIGINAL SOURCE:
      ORGANIOM. Zea mays
     IMMEDIATE SOURCE:
     CLONE: P12218
    FEATURE:
      NAME/KEY: CDS
      LOCATION: 126..983
JS-09-412-102-4
 grainy Matinto
                         1 79 Comer (6) 190 4: 1 Spring h 1925;
 Best Local Similarity 100.0%; Pred. No. 6.5e-06;
 Matches 35: Conservative 6: Mismatches C: Indels 0: Gaps
Qy 2064 ttqааааааааааааааааааааааааааа 2698
       Db 1200 IIIJAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1324
RESULT 15
US-09-217-787-1
; Sequence 3, Application JS/09217787
; Patent No. 6284948
GENERAL INFORMATION:
    APPLICANT: JESSEN, HOLLY J
    APPLICANT: MEYER, TERRY E
    TITLE OF INVENTION. SIMES AND METHODS FOR CONTROL OF
TITLE OF INVENTION. MEMATORS IN PLANTS
NUMBER OF SEQUENCES: 10
    CORRESPONDENCE ADDRESS:
      ADDRESSEE: W. Murray Spruill (Aloton & Bird, LLP)
      STREET: 3605 Glenwood Ave. suite 310
      CITY: Raliegh
      STATE: NO
      COUNTRY: US
      ZIP: 27622
    COMPUTER READABLE FORM:
      MEDIUM TYPE. Ploppy disk
      COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC DOS/MS-DOS
      SOFTWARE. Fated in Release #1.0. Version #1.00
    CURRENT APPLICATION DATA:
```

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- APPSICALL N. NUMBER: - US/09/21/,787
      FILLING GALES
       CLASSIC PALL NO
    ALL GENEY ACTIONS ONE GEMALICALS
      NAME: Opruiil, W. Murray
      FEGISTRATION NUMBER: 32,7443
BEDERESCHINGERET NUMBER: 5718 DART
    TELECOMM NECAL ON INFORMATIONS
      THILEPH NE. (19.420-2202)
      TELEFAX: 91 (881 3175)
   INFORMATION FOR JOG TO NOT SE
    SELUTION THAFA LERGISLICS:
      TENGTH 132' base pairs
       TYPE: nothernacid.
      TIRANI DNESS pingle
      - 1 deale iv - Linear
    M(\mathrm{GLEPULE}) = \mathrm{CYPE}_{\mathrm{T}} = \mathrm{cPNA}
     HELLINAL COURTES
     HOGANI'M. Zosa mays
    IMMEDIAL SOURCES.
    EEALURE
     NAMEZELY: C.::
      - 1200 ATT | No. | 1200 2008 C
M. 594 . 1 1 78 1 3
 Martches () Conservative () Mismarches () Indels () Gaps ():
\zeta\gamma=2004 , the resistant randomagnatic and associated as 2098
      Faurch completed: May 1.6, 2002, 21:23:39 \pm 1.6 times \pm 82. Lee
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